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Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 M QNWATFQOKHHIINTPIICNTIMDNNNIYVGGCKRVNTFISSATTVAICTGVINNNV 60
Db 1 M QNWATFQOKHHIINTPIICNTIMDNNNIYVGGCKRVNTFISSATTVAICTGVINLV 60
QY 61 LSTTRFQNLNCTRTSITPRPCPYSSRSTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNLNCTRTSITPRPCPYSSRSTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 9
US-09-948-391A-22
; Sequence 22, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; PRIORITY FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at
; OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
; OTHER INFORMATION: (recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6)
US-09-948-391A-22

Query Match 99.0%; Score 601; DB 10; Length 117;
Best Local Similarity 98.2%; Pred. No. 1.2e-60;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Db 7 M QNWATFQOKHHIINTPIICNTIMDNNNIYVGGCKRVNTFISSATTVAICTGVINLV 66
QY 61 LSTTRFQNLNCTRTSITPRPCPYSSRSTETNYICVKCENQYPVHFAGIGRCP 111
Db 67 LSTTRFQNLNCTRTSITPRPCPYSSRSTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 10
US-09-961-400-22
; Sequence 22, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641

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; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-26

Query Match
Best Local Similarity 99.2%; Score 602; DB 10; Length 111;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 6
US-09-948-391A-17
; Sequence 17, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; TITLE OF INVENTION: Department of Health and Human Services
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1,
; OTHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant
; OTHER INFORMATION: Met(-1) RacOR1 Met22Leu Met57Leu)
US-09-948-391A-21

Query Match
Best Local Similarity 99.0%; Score 601; DB 10; Length 111;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 7
US-09-948-391A-21
; Sequence 21, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; TITLE OF INVENTION: Department of Health and Human Services
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: (recombinant Met(-1) RacOR1)
US-09-948-391A-17

Query Match
Best Local Similarity 99.0%; Score 601; DB 10; Length 111;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
Db 1 MGNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 8
US-09-961-400-21
; Sequence 21, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-21

Query Match
Best Local Similarity 99.0%; Score 601; DB 10; Length 111;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Query Match 99.2%; Score 602; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 8.4e-61;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 62 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 4

US-09-948-391A-26
; Sequence 26, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: and Gln2ser substitution (Met (-1) RacOR1 Q1S)
US-09-948-391A-26

Query Match 99.2%; Score 602; DB 10; Length 111;
Best Local Similarity 99.1%; Pred. No. 8.5e-61;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 5

US-09-961-400-26
; Sequence 26, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613

RESULT 2

US-09-948-391A-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana oocyte ribonuclease (RacOR1) synthetic
; OTHER INFORMATION: Gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match 99.2%; Score 602; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 8.4e-61;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 QNWATFOQKHINTPIICNTMDNNIYVGGQCKRVNTFISSATTYKAITGVINNNVL 60
QY 62 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
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RESULT 3

US-09-961-400-15
; Sequence 15, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-15

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:40 ; Search time 35.6155 Seconds
(without alignments)
865.070 Million cell updates/sec

Title: US-09-961-400-17
Perfect score: 607
Sequence: 1 MONWATFOQKHINTPICNICVKENQYPVHFAGIGRCP 111

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Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	602	99.2	110	10	US-09-948-391A-15
3	602	99.2	110	10	US-09-961-400-15
4	602	99.2	111	10	US-09-948-391A-26
5	602	99.2	111	10	US-09-961-400-26
6	601	99.0	111	10	US-09-948-391A-17
7	601	99.0	111	10	US-09-948-391A-21
8	601	99.0	111	10	US-09-961-400-21
9	601	99.0	117	10	US-09-948-391A-22
10	601	99.0	117	10	US-09-961-400-22
11	597	98.4	110	10	US-09-948-391A-24
12	597	98.4	110	10	US-09-961-400-24
13	596	98.2	110	10	US-09-961-400-19
14	590	97.2	110	10	US-09-948-391A-19
15	286.5	47.2	105	10	US-09-948-391A-6

16	286.5	47.2	105	10	US-09-961-400-6	Sequence 6, Appli
17	283.5	46.7	111	10	US-09-961-400-9	Sequence 9, Appli
18	282.5	46.5	105	14	US-10-153-882-2	Sequence 2, Appli
19	281.5	46.4	104	10	US-09-961-400-2	Sequence 2, Appli
20	281.5	46.4	105	10	US-09-948-391A-13	Sequence 13, Appli
21	281.5	46.4	105	10	US-09-961-400-13	Sequence 13, Appli
22	281.5	46.4	105	10	US-09-948-391A-28	Sequence 28, Appli
23	281.5	46.4	127	10	US-09-961-400-28	Sequence 28, Appli
24	280.5	46.2	104	10	US-09-948-391A-2	Sequence 2, Appli
25	280.5	46.2	105	10	US-09-961-400-8	Sequence 8, Appli
26	276.5	45.6	104	10	US-09-948-391A-11	Sequence 11, Appli
27	276.5	45.6	104	10	US-09-961-400-11	Sequence 11, Appli
28	275.5	45.4	104	10	US-09-948-391A-4	Sequence 4, Appli
29	275.5	45.4	104	10	US-09-961-400-4	Sequence 4, Appli
30	272.5	44.9	104	9	US-09-986-119-1	Sequence 1, Appli
31	272.5	44.9	104	10	US-09-918-887-1	Sequence 1, Appli
32	271.5	44.7	105	10	US-09-948-391A-8	Sequence 8, Appli
33	271.5	44.7	111	10	US-09-948-391A-9	Sequence 9, Appli
34	269.5	44.4	104	12	US-10-461-713-53	Sequence 53, Appli
35	206	33.9	83	9	US-09-986-119-3	Sequence 3, Appli
36	206	33.9	83	10	US-09-918-887-3	Sequence 3, Appli
37	163	26.9	169	13	US-10-016-447-2	Sequence 2, Appli
38	135.5	22.3	124	12	US-10-037-417-103	Sequence 103, App
39	131.5	21.7	119	12	US-10-016-248-89	Sequence 89, Appli
40	131.5	21.7	119	15	US-10-074-978A-139	Sequence 139, App
41	121	19.9	99	15	US-10-074-978A-141	Sequence 141, App
42	117.5	19.4	124	12	US-10-461-713-52	Sequence 52, Appli
43	117	19.3	147	9	US-09-731-872-254	Sequence 254, App
44	117	19.3	147	10	US-09-876-997-254	Sequence 254, App
45	114.5	18.9	124	9	US-09-981-286A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-961-400-17
; Sequence 17, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-17

Query Match 100.0%; Score 607; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.3e-61;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MONWATFOQKHINTPICNIMNNIYVGQCKRVNTFISSATTVAICTGVINMV 60
Db 1 MONWATFOQKHINTPICNIMNNIYVGQCKRVNTFISSATTVAICTGVINMV 60
Qy 61 LSTRFQNTCTRTSITPRCPYSSRTETNYICVKENQYPVHFAGIGRCP 111
Db 61 LSTRFQNTCTRTSITPRCPYSSRTETNYICVKENQYPVHFAGIGRCP 111


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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-61

Query Match 45.7%; Score 277.5; DB 3; Length 254;
Best Local Similarity 49.1%; Pred. No. 2.2e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

QY 1 MONWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
DB 1 MSDWLTFOQKHITNTRDVCNDIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASK 56
QY 59 NVLSTTRFOLNCTRTSITRCPYSSRTETNYICVKCENQYVHFAGIGRC 110
DB 57 NVLTISEFYLSDC---NVTSRCKYKLKSTNKFVTCENQAPVHFVGVGSC 105

RESULT 15
US-08-875-811-49
; Sequence 49, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997

;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-49

Query Match 45.7%; Score 277.5; DB 3; Length 355;
Best Local Similarity 49.1%; Pred. No. 3.3e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

QY 1 MONWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
DB 251 MSDWLTFOQKHITNTRDVCNDIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASK 306
QY 59 NVLSTTRFOLNCTRTSITRCPYSSRTETNYICVKCENQYVHFAGIGRC 110
DB 307 NVLTISEFYLSDC---NVTSRCKYKLKSTNKFVTCENQAPVHFVGVGSC 355

Search completed: May 7, 2004, 21:40:45
Job time : 12.8756 secs
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QY 59 NVLSTTRFQKHIINT-PIICNTIMDNIIYVGGCKRVNTFIISATTVKAICTGVI-NM 110
Db 64 NVLTSEFYLSDC---NVTSRPKYKLLKSTNKFVCVCENQAPVHFVGVGSC 112

RESULT 12

US-08-875-811-63
; Sequence 63, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-63

Query Match 45.7%; Score 277.5; DB 3; Length 129;
Best Local Similarity 49.5%; Pred. No. 9.6e-25;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
QY 2 QNWATFQKHIINT-PIICNTIMDNIIYVGGCKRVNTFIISATTVKAICTGVI-NMN 59
Db 26 QDWLTFQKXHIINT-PIICNTIMDNIIYVGGCKRVNTFIISATTVKAICTGVI-NMN 81
QY 60 VLSSTTRFQKHIINT-PIICNTIMDNIIYVGGCKRVNTFIISATTVKAICTGVI-NMN 110
Db 82 VLTSEFYLSDC---NVTSRPKYKLLKSTNKFVCVCENQAPVHFVGVGSC 129

RESULT 13

US-08-875-811-59
; Sequence 59, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.

; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-59

Query Match 45.7%; Score 277.5; DB 3; Length 251;
Best Local Similarity 49.1%; Pred. No. 2.2e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;
QY 1 QMWATFQKHIINT-PIICNTIMDNIIYVGGCKRVNTFIISATTVKAICTGVI-NM 58
Db 147 MSDWLTQKXHIINT-PIICNTIMDNIIYVGGCKRVNTFIISATTVKAICTGVI-NM 202
QY 59 NVLSTTRFQKHIINT-PIICNTIMDNIIYVGGCKRVNTFIISATTVKAICTGVI-NM 110
Db 203 NVLTSEFYLSDC---NVTSRPKYKLLKSTNKFVCVCENQAPVHFVGVGSC 251

RESULT 14

US-08-875-811-61
; Sequence 61, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

```
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ran, David B.
; REGISTRATION NUMBER: 38,589
; REFERENCE/DOCKET NUMBER: 15280-267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-626-288-1

Query Match      45.7%; Score 277.5; DB 4; Length 104;
Best Local Similarity 49.5%; Pred. No. 7.4e-25;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 59
Db 1 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

QY 60 VLSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 110
Db 57 VLATSEFYLSDC--NVTSPCKYKLGKSTNKFVCVTENQAPVHFVGVGSC 104

RESULT 10
US-09-095-429-1
; Sequence 1, Application US/09095429
; Patent No. 6649393
; GENERAL INFORMATION:
; APPLICANT: Youle, Richard
; APPLICANT: Vasandani, Veena
; APPLICANT: Wu, Yon-Neng
; APPLICANT: Boix, Ester
; APPLICANT: Argelt, Wojetech
; TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
; TITLE OF INVENTION: Allows Production by Recombinant Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,429
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/626,288
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ran, David B.
; REGISTRATION NUMBER: 38,589
; REFERENCE/DOCKET NUMBER: 15280-267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-095-429-1

Query Match      45.7%; Score 277.5; DB 4; Length 104;
Best Local Similarity 49.5%; Pred. No. 7.4e-25;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 59
Db 1 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

QY 60 VLSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 110
Db 57 VLATSEFYLSDC--NVTSPCKYKLGKSTNKFVCVTENQAPVHFVGVGSC 104

RESULT 11
US-08-875-811-32
; Sequence 32, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02568
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-32

Query Match      45.7%; Score 277.5; DB 3; Length 112;
Best Local Similarity 49.1%; Pred. No. 8.1e-25;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 8 MSDWLTFFQKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 63
```

APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-51

Query Match 46.0%; Score 279.5; DB 3; Length 358;
Best Local Similarity 49.1%; Pred. No. 2e-24;
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

Qy 1 MNWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-NM 58
Db 1 MEDWLTFOQKHINTRDVDCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 56

Qy 59 NVLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCNOYPVHFAGIGRC 110
Db 57 VLTITSEFYSLDC---NVTSRPCKYKLNKSTNKFVTCENQAPVHFVGVGSC 105

RESULT 7
US-09-394-268-1
Sequence 1, Application US/09394268
Patent No. 6175003
GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF MAKING THEM
FILE REFERENCE: 5013
CURRENT APPLICATION NUMBER: US/09/394,268
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 1
LENGTH: 104
TYPE: PRT
ORGANISM: Rana pipiens
US-09-394-268-1

Query Match 45.7%; Score 277.5; DB 3; Length 104;

Best Local Similarity 49.5%; Pred. No. 7.4e-25;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
Qy 2 QNWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59
Db 1 QDWLTFQKHINTRDVDCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56
Qy 60 VLSSTRFQNLCTRTSITPRPCPYSSRTETNYICVKCNOYPVHFAGIGRC 110
Db 57 VLTITSEFYSLDC---NVTSRPCKYKLNKSTNKFVTCENQAPVHFVGVGSC 104

RESULT 8
US-09-687-748-1
Sequence 1, Application US/09687748
Patent No. 6423515
GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
FILE REFERENCE: 5013 US.01
CURRENT APPLICATION NUMBER: US/09/687,748
CURRENT FILING DATE: 2000-10-14
PRIOR APPLICATION NUMBER: 09/394,268
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 1
LENGTH: 104
TYPE: PRT
ORGANISM: Rana pipiens
US-09-687-748-1

Query Match 45.7%; Score 277.5; DB 4; Length 104;
Best Local Similarity 49.5%; Pred. No. 7.4e-25;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 2 QNWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59
Db 1 QDWLTFQKHINTRDVDCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

Qy 60 VLSSTRFQNLCTRTSITPRPCPYSSRTETNYICVKCNOYPVHFAGIGRC 110
Db 57 VLTITSEFYSLDC---NVTSRPCKYKLNKSTNKFVTCENQAPVHFVGVGSC 104

RESULT 9
US-08-626-288-1
Sequence 1, Application US/08626288
Patent No. 6649392
GENERAL INFORMATION:
APPLICANT: Youle, Richard
APPLICANT: Vasandani, Veena
APPLICANT: Wu, Yon-Neng
APPLICANT: Boix, Ester
APPLICANT: Ardelet, Wojciech
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which Allows Production by Recombinant Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,288
FILING DATE: No. 6649392 yet assigned

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DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-2

Query Match
Best Local Similarity 46.9%; Score 284.5; DB 1; Length 104;
Matches 55; Conservative 16; Mismatches 31; Indels 9; Gaps 4;

QY 2 QNWTATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 59
Db 1 EDMLTFQKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

QY 60 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCNQYPVHFAGIGRC 110
Db 57 VLITSEFYLSDC---NVTSPCKYKLLKSTNKFCTVCENQAPVHFVGVGSC 104

RESULT 4
US-08-875-811-39
; Sequence 39, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-39

Query Match
Best Local Similarity 46.0%; Score 279.5; DB 3; Length 105;
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 MNWTATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 1 EDMLTFQKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 56

QY 59 NVLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCNQYPVHFAGIGRC 110
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Db 57 NVLITSEFYLSDC---NVTSPCKYKLLKSTNKFCTVCENQAPVHFVGVGSC 105

RESULT 5
US-08-875-811-41
; Sequence 41, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-41

Query Match
Best Local Similarity 46.0%; Score 279.5; DB 3; Length 355;
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 MNWTATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 251 MEDWLTFOQKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 306

QY 59 NVLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCNQYPVHFAGIGRC 110
Db 307 NVLITSEFYLSDC---NVTSPCKYKLLKSTNKFCTVCENQAPVHFVGVGSC 355

RESULT 6
US-08-875-811-51
; Sequence 51, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
```

```

; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
; OTHER INFORMATION: /note= "Frog Lectin from Rana
; catesbeiana"
; US-08-891-848-12

Query Match 97.0%; Score 588.5; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 6.6e-61;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

; OTHER INFORMATION: /note= "Frog Lectin from Rana
; catesbeiana"
; US-08-891-848-12

Query Match 97.0%; Score 588.5; DB 3; Length 111;
Best Local Similarity 98.2%; Pred. No. 6.6e-61;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 QNWATFOQKHIIINTPII-CNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVINMV 60
Db 1 ENWATFOQKHIIINTPII-CNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVINMV 60
QY 61 LSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D, Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; TELEX: No. 5728805 Applicable
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:28:45 ; Search time 12.8756 Seconds
(without alignments)
445.066 Million cell updates/sec

Title: US-09-961-400-17
Perfect score: 607
Sequence: 1 MQNWATFQXKHINTPICN.....ICVKENQYDPVHAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/protdata/2/iaa/5B COMB.pep.*
3: /cgn2_6/protdata/2/iaa/6A COMB.pep.*
4: /cgn2_6/protdata/2/iaa/6B COMB.pep.*
5: /cgn2_6/protdata/2/iaa/PCTUS COMB.pep.*
6: /cgn2_6/protdata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	588.5	97.0	111	2	US-08-891-848-12
2	588.5	97.0	111	3	US-08-875-811-8
3	284.5	46.9	104	1	US-08-467-955-2
4	279.5	46.0	105	3	US-08-875-811-39
5	279.5	46.0	355	3	US-08-875-811-41
6	279.5	46.0	358	3	US-08-875-811-51
7	277.5	45.7	104	3	US-09-394-268-1
8	277.5	45.7	104	4	US-09-687-748-1
9	277.5	45.7	104	4	US-08-626-288-1
10	277.5	45.7	104	4	US-09-095-429-1
11	277.5	45.7	112	3	US-08-875-811-32
12	277.5	45.7	129	3	US-08-875-811-63
13	277.5	45.7	251	3	US-08-875-811-59
14	277.5	45.7	254	3	US-08-875-811-61
15	277.5	45.7	355	3	US-08-875-811-49
16	277.5	45.7	355	3	US-08-875-811-57
17	277.5	45.7	355	3	US-08-875-811-64
18	277.5	45.7	366	3	US-08-875-811-55
19	277.5	45.7	379	3	US-08-875-811-43
20	274.5	45.2	104	1	US-08-283-971-1
21	274.5	45.2	104	1	US-07-921-619-1
22	274.5	45.2	104	1	US-08-467-955-1
23	274.5	45.2	104	2	US-08-891-848-13
24	272.5	44.9	104	3	US-08-875-811-1
25	272.5	44.9	104	3	US-09-394-268-2
26	272.5	44.9	104	4	US-09-071-672-1
27	272.5	44.9	104	4	US-09-687-748-2

28 272.5 44.9 104 4 US-09-986-119-1 Sequence 1, Appli
29 272.5 44.9 105 3 US-08-875-811-26 Sequence 26, Appl
30 272.5 44.9 106 3 US-08-875-811-28 Sequence 28, Appl
31 272.5 44.9 107 3 US-08-875-811-30 Sequence 30, Appl
32 271.5 44.7 105 3 US-08-875-811-24 Sequence 24, Appl
33 269.5 44.4 104 4 US-08-626-288-2 Sequence 2, Appli
34 269.5 44.4 104 4 US-09-095-429-2 Sequence 2, Appli
35 268.5 44.2 358 3 US-08-875-811-45 Sequence 45, Appl
36 268.5 44.2 365 3 US-08-875-811-37 Sequence 53, Appl
37 250.5 41.3 107 3 US-08-875-811-20 Sequence 20, Appl
38 239.5 39.5 111 3 US-08-875-811-22 Sequence 22, Appl
39 236 38.9 114 3 US-09-223-118-3 Sequence 3, Appli
40 232.5 38.3 360 3 US-08-875-811-47 Sequence 47, Appl
41 227 37.4 114 3 US-09-223-118-2 Sequence 2, Appli
42 226 37.2 114 3 US-09-223-118-1 Sequence 1, Appli
43 225 37.1 114 3 US-09-223-118-4 Sequence 4, Appli
44 206 33.9 83 3 US-08-875-811-2 Sequence 2, Appli
45 206 33.9 83 4 US-09-071-672-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-891-848-12
; Sequence 12, Application US/08891848
; Patent No. 5955073
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Youle, Richard J.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Nicholls, Peter J.
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,848
; FILING DATE: No. 5955073 yet assigned
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,462
; FILING DATE: 22-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/014,082
; FILING DATE: 04-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,195
; FILING DATE: 22-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/510,696
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-11031005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid

XX AC AAY28865;
 XX DT 25-JAN-2000 (first entry)
 XX DE Rana pipiens liver ribonuclease (RaPLR1).
 XX DE Rana pipiens liver ribonuclease; RaPLR1; covalently bound; LL2 antibody;
 XX KW ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog;
 XX KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase;
 XX KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
 XX OS Rana pipiens.
 XX PN WO9950398-A2.
 XX PD 07-OCT-1999.
 XX PF 26-MAR-1999; 99WO-US006641.
 XX PR 27-MAR-1998; 98US-0079751P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Rybak SM, Newton DL;
 XX DR WPI; 1999-610847/52.
 XX DR N-PSDB; AAZ08124.
 XX FT New recombinant ribonucleases, used for killing target cells, e.g. for
 XX FT treating cancers, viral infections or autoimmune diseases.
 XX PS Claim 1; Page 55; 71pp; English.
 XX CC The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein.
 XX CC Carboxy terminal end of RaPLR1 has a covalently bound ligand binding
 XX CC moiety, which can be a LL2 antibody directed against CD22 on cancerous B
 XX CC cells or human chorionic gonadotrophin (hCG) effective against Kaposi's
 XX CC Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria
 XX CC without an N-terminal methionine due to the presence of a signal peptide
 XX CC that is cleaved by bacteria. The soluble expression of ribonuclease
 XX CC allows the proteins to be fused in-frame with ligand binding moieties to
 XX CC form cytotoxic fusion proteins. They can be used for treatment of cancer
 XX CC and autoimmune diseases
 XX SQ Sequence 104 AA;
 Query Match 46.4%; Score 281.5; DB 2; Length 104;
 Best Local Similarity 49.5%; Pred. No. 2.9e-24;
 Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
 QY 2 QNWATFOOKHILNT-PIICNTIMDNIIYVGQCKRVNTFISSATTVAICTGVI-NMN 59
 Db 1 QDWLTFQKKHLNTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGHIASKN 56
 QY 60 VLSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRC 110
 Db 57 VLTITSEFYLSDC--NVTISRCKYKLLKSTNTFCVTCENQAPVHFVGVC 104
 RESULT 13
 AAY28871
 ID AAY28871 standard; protein; 105 AA.
 XX AC AAY28871;
 XX DT 25-JAN-2000 (first entry)
 XX DE Recombinant Met(-1) RaPLR1 Gln1Ser amino acid sequence.
 XX KW Recombinant Met(-1) Rana pipiens ribonuclease Gln1Ser; RaPLR1; CD22;
 XX KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 XX KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;

KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
 KW autoimmune disease; RNase.
 XX OS Rana pipiens.
 XX OS Synthetic.
 XX FT Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RaPLR1"
 FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"
 XX PN WO9950398-A2.
 XX PD 07-OCT-1999.
 XX PF 26-MAR-1999; 99WO-US006641.
 XX PR 27-MAR-1998; 98US-0079751P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Rybak SM, Newton DL;
 XX DR WPI; 1999-610847/52.
 XX DR N-PSDB; AAZ08129.
 XX FT New recombinant ribonucleases, used for killing target cells, e.g. for
 XX FT treating cancers, viral infections or autoimmune diseases.
 XX PS Claim 34; Page 61; 71pp; English.
 XX CC The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
 XX CC protein with Met at position 1 and Gln2Ser. Carboxy terminal end of
 XX CC recombinant RaPLR1 has a covalently bound ligand binding moiety, which
 XX CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
 XX CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
 XX CC Recombinant ribonucleases can be expressed in bacteria without an N-
 XX CC terminal methionine due to the presence of a signal peptide that is
 XX CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 XX CC proteins to be fused in-frame with ligand binding moieties to form
 XX CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 XX CC autoimmune diseases
 XX SQ Sequence 105 AA;
 Query Match 46.4%; Score 281.5; DB 2; Length 105;
 Best Local Similarity 49.1%; Pred. No. 3e-24;
 Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;
 QY 1 MQNWATFOOKHILNT-PIICNTIMDNIIYVGQCKRVNTFISSATTVAICTGVI-NM 58
 Db 1 MSDWLTFOKKHLNTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGHIASK 56
 QY 59 NVLSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRC 110
 Db 57 NVLTITSEFYLSDC--NVTISRCKYKLLKSTNTFCVTCENQAPVHFVGVC 105
 RESULT 14
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 ID AAY28879 standard; protein; 127 AA.
 XX AC AAY28879;
 XX DT 25-JAN-2000 (first entry)
 XX DE Rana pipiens Clone 5alb ribonuclease.
 XX KW Rana pipiens ribonuclease Clone 5alb; RaPLR1; covalently bound; RNase;
 XX KW LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase;
 XX KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; cancer;
 XX KW recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;

```
ID AAY28869 standard; protein; 105 AA.
XX
AC AAY28869;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein.
XX
KW Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RaPLR1;
XX CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase;
XX KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
XX KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
XX KW cancer; frog; autoimmune disease.
XX
OS Rana pipiens.
OS Synthetic.
OS
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "Met not found in wild type RaPLR1"
FT Misc-difference 1
FT /note= "(His)6 histidine tag attached to N-terminal Met"
FT Misc-difference 24
FT /note= "wild type Met replaced with Leu"
FT
XX WO9950398-A2.
XX
XX 07-OCT-1999.
XX
XX 26-MAR-1999; 99WO-US006641.
XX
XX 27-MAR-1998; 98US-0079751P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Rybak SM, Newton DL;
XX
XX WPI; 1999-610847/52.
XX N-PSDB; AA208127.
XX
XX New recombinant ribonucleases, used for killing target cells, e.g. for
XX treating cancers, viral infections or autoimmune diseases.
XX
XX Claim 4; Page 59; 7lpp; English.
XX
XX The present sequence is a recombinant Rana pipiens ribonuclease protein
XX (RaPLR1) with Met at position 1 attached to (His)6 tag and Met24Leu
XX Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand
XX binding moiety, which can be a LL2 antibody directed against CD22 on
XX cancerous B cells or human chorionic gonadotrophin (hCG) effective
XX against Kaposi's sarcoma cells. Recombinant ribonucleases can be
XX expressed in bacteria without an N-terminal methionine due to the
XX presence of a signal peptide that is cleaved by bacteria. The soluble
XX expression of ribonuclease allows the proteins to be fused in-frame with
XX ligand binding moieties to form cytotoxic fusion proteins. They can be
XX used for treatment of cancer and autoimmune diseases
XX
SQ Sequence 105 AA;
Query Match 46.7%; Score 283.5; DB 2; Length 105;
Best Local Similarity 49.1%; Pred.No.1.7e-24;
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;
QY 1 MQNWATFOOKHIINT-PIICNTIMDNIIYVGQCKRVNTFIISATTVKACTGVI-NM 58
DB 1 MQDWLTFQKHLINTRDVCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGLIASK 56
QY 59 NVLSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCNQYVPHFAGIGRC 110
DB 57 NVLTSEFYLSDC---NVTSRPCYKYLKSKTNTFCVTCENQAPVHFVGVGHC 105
RESULT 11
AAY28865
ID AAY28865 standard; protein; 104 AA.
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```
AAAY39400
ID AAY39400 standard; protein; 105 AA.
XX
AC AAY39400;
XX
DT 01-DEC-1999 (first entry)
XX
DE Recombinant frog Onconase.
XX
KW Ribonuclease; protein synthesis; inhibition; cancer; cytotoxic.
XX
OS Rana pipiens.
XX
XX WO9946389-A1.
XX
XX 16-SEP-1999.
XX
XX 11-MAR-1999; 99WO-US004252.
XX
XX 11-MAR-1998; 98US-0077557P.
XX (IMMU-) IMMUNOMEDICS INC.
XX
XX Goldenberg DM, Hansen H, Leung S;
XX
XX WPI; 1999-551416/46.
XX N-PSDB; AA219767.
XX
XX A new recombinant Onconase used to treat, e.g. colon cancer.
XX
XX Example 1; Fig 1; 42pp; English.
XX
XX This sequence represents recombinant frog Onconase. Onconase has
XX ribonuclease and anti-tumour activity. The cDNA was produced via PCR
XX (using primers AA219768-Z19769) of two synthetic DNAs whose sequences
XX encoded most of the N-terminal or the C-terminal amino acids of mature
XX Onconase. The two PCR products generated encoded either the N-terminal 54
XX amino acids (minus the initial methionine) or the C-terminal 51 amino
XX acids, and were ligated in frame at an NruI site. The cDNA was then
XX subcloned into a vector e.g., pBluescript, where the ATG initiation codon
XX was ligated to the cDNA. After expression in E. coli, the recombinant
XX protein was purified. The initial N-formyl methionine was cleaved off and
XX the now N-terminal glutamate residue cyclised to form an N-terminal
XX pyroglutamate. The pyroglutamate residue forms part of the phosphate
XX binding pocket of Onconase and is essential for both ribonuclease and anti-
XX tumour activity. Onconase is a 12 kD ribonuclease which causes cell
XX death as a result of potent inhibition of protein synthesis by a
XX mechanism involving inactivation of cellular RNA. It is not inhibited by
XX mammalian placental ribonuclease inhibitor, which may explain its
XX enhanced cytotoxicity relative to mammalian enzymes. It has anti-tumour
XX activity against a variety of solid tumours e.g. colon or pancreatic
XX cancers, and can be used alone or in combination with other anti-cancer
XX agents such as tamoxifen. When used as an anti-tumour agent, Onconase can
XX be conjugated to a marker which targets it to a specific cell type
XX
SQ Sequence 105 AA;
Query Match 46.5%; Score 282.5; DB 2; Length 105;
Best Local Similarity 50.0%; Pred.No.2.3e-24;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
QY 1 MQNWATFOOKHIINT-PIICNTIMDNIIYVGQCKRVNTFIISATTVKACTGVI-NM 58
DB 1 MQDWLTFQKHLINTRDVCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGLIASK 56
QY 59 NVLSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCNQYVPHFAGIGRC 110
DB 57 NVLTSEFYLSDC---NVTSRPCYKYLKSKTNTFCVTCENQAPVHFVGVGSC 105
RESULT 12
AAY28865
ID AAY28865 standard; protein; 104 AA.
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CC (Rana catesbeiana) lectin used to describe the method of the invention
 XX Sequence 111 AA;
 SQ

Query Match 97.0%; Score 588.5; DB 2; Length 111;
 Best Local Similarity 98.2%; Pred. No. 2.2e-59;
 Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 QNWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
 Db 1 ENWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

QY 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
 Db 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 8
 AAY28867
 ID AAY28867 standard; protein; 105 AA.
 AC AAY28867;
 XX 25-JAN-2000 (first entry)
 DT Recombinant Met (-1) RaPLR1.
 DE
 XX Recombinant Met (-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase;
 KW covalently bound; IL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
 KW autoimmune disease.
 XX
 OS Rana pipiens.
 OS Synthetic.

Key Location/Qualifiers
 FH Misc-difference 1 /note= "Met not found in wild type RaPLR1"
 FT
 XX WO9950398-A2.
 XX 07-OCT-1999.
 XX 26-MAR-1999; 99WO-US006641.
 XX 27-MAR-1998; 98US-0079751P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Rybak SM, Newton DL;
 XX WPI; 1999-610847/52.
 XX N-PSDB; AAZ08126.
 XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.
 XX
 PS Claim 34; Page 57; 7lpp; English.
 XX
 CC The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
 CC protein with Met at position 1. Carboxy terminal end of recombinant
 CC RaPLR1 has a covalently bound ligand binding moiety, which can be a IL2
 CC antibody directed against CD22 on cancerous B cells or human chorionic
 CC gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant
 CC ribonucleases can be expressed in bacteria without an N-terminal
 CC methionine due to the presence of a signal peptide that is cleaved by
 CC bacteria. The soluble expression of ribonuclease allows the proteins to
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
 CC proteins. They can be used for treatment of cancer and autoimmune
 CC diseases
 XX
 SQ Sequence 105 AA;

Query Match 47.2%; Score 286.5; DB 2; Length 105;
 Best Local Similarity 50.0%; Pred. No. 7.9e-25;
 Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 MONWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
 Db 1 MODWLTFOQKHINTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 56

QY 59 NVLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
 Db 57 NVLTSEFYLSDC---NVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

RESULT 9
 AAW06544
 ID AAW06544 standard; protein; 104 AA.
 XX
 AC AAW06544;
 XX 22-AUG-1997 (first entry)
 DT
 XX Antitumour protein from Rana pipiens oocytes.
 DE Tumour; chemotherapy; radiotherapy; frog.
 KW
 XX Rana pipiens.
 OS
 PN WO9639428-A1.
 XX 12-DEC-1996.
 PD
 XX 03-JUN-1996; 96WO-US008304.
 PF
 XX 06-JUN-1995; 95US-00467955.
 XX (ALFA-) ALFACELL CORP.
 XX Ardelit WJ;
 XX WPI; 1997-043063/04.
 XX Antitumour proteins from Rana pipiens oocyte(s) - have fewer
 XX disadvantages than chemotherapy, surgery and radiotherapy.
 PT
 XX Claim 8; Page 28; 45pp; English.
 PS
 XX The present sequence is a specifically claimed example of an antitumour
 CC protein from the generic protein in AAW18224, with the molecular weight
 CC 12000. This is one of two preferred proteins (the other in AAW06543) that
 CC have been isolated from Rana pipiens oocytes. Both proteins have a
 CC blocked amino terminal group and are essentially free of carbohydrates.
 CC The proteins are used to treat tumours. Use of the peptides has fewer
 CC disadvantages than chemotherapy, radiotherapy and surgery in the
 CC treatment of tumours
 XX
 SQ Sequence 104 AA;

Query Match 46.9%; Score 284.5; DB 2; Length 104;
 Best Local Similarity 49.5%; Pred. No. 1.3e-24;
 Matches 55; Conservative 16; Mismatches 31; Indels 9; Gaps 4;

QY 2 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 59
 Db 1 EDWLTFOQKHINTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

QY 60 VLSSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
 Db 57 VLTSEFYLSDC---NVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGRC 104

RESULT 10
 AAY28869

SQ Sequence 110 AA;

Query Match 98.4%; Score 597; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 2.3e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NWAIFQOKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMNVLS 62
DB 2 NWAIFQOKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMNVLS 61

QY 63 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 62 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 6
AAI28874
ID AAY28874 standard; protein; 110 AA.
AC AAY28874;
XX
XX
XX 25-JAN-2000 (first entry)
XX
XX Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.
DE
XX
XX Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound;
KW RaCOR1 Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22;
KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;
KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW cancer; bullfrog; RNase; autoimmune disease.
XX
OS Rana catesbeiana.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 22 /note= "Wild type Met replaced with Leu"
FT FT
FT Misc-difference 57 /note= "Wild type Met replaced with Leu"
FT FT
XX WO9950398-A2.
XX
XX 07-OCT-1999.
XX
XX 26-MAR-1999; 99WO-US006641.
XX
XX 27-MAR-1998; 98US-0079751P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Rybak SM, Newton DL;
XX
XX WPI; 1999-610847/52.
XX
XX DR N-PSDB; AAZ08132.
XX
XX
XX New recombinant ribonucleases, used for killing target cells, e.g. for
XX treating cancers, viral infections or autoimmune diseases.
XX
XX Claim 22; Page 64; 71pp; English.
XX
XX The present sequence is a recombinant Rana catesbeiana oocyte
XX ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal
XX end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
XX which can be a LL2 antibody directed against CD22 on cancerous B cells or
XX human chorionic gonadotropin (hCG) effective against Kaposi's sarcoma
XX cells. Recombinant ribonucleases can be expressed in bacteria without an
XX N-terminal methionine due to the presence of a signal peptide that is
XX cleaved by bacteria. The soluble expression of ribonuclease allows the
XX proteins to be fused in-frame with ligand binding moieties to form
XX cytotoxic fusion proteins. They can be used for treatment of cancer and
XX autoimmune diseases
XX
XX Sequence 110 AA;

Query Match 98.2%; Score 596; DB 2; Length 110;
Best Local Similarity 98.2%; Pred. No. 3e-60;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMNVLS 61
DB 1 QNWATFOQKHIIINTPIICNTILDNIIYVGGQCKRVNTFISSATTVKAICTGVINMNVLS 60

QY 62 STRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 61 STRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 7
AAY33321
ID AAY33321 standard; protein; 111 AA.
AC AAY33321;
XX
XX 29-NOV-1999 (first entry)
XX
XX Frog lectin protein fragment.
DE
XX
XX Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;
KW heavy chain; cell surface marker; treatment; tumor; viral infection;
KW parasite infection; immune dysfunctional cell; autoimmune disease;
KW contraceptive; cell separation; transplantation; bone marrow ablation;
KW leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
XX
OS Rana catesbeiana.
XX
XX US5955073-A.
XX
XX 21-SEP-1999.
XX
XX 09-JUL-1997; 97US-00891848.
XX
XX 20-APR-1990; 90US-00510696.
XX PR 22-OCT-1991; 91US-00779195.
XX PR 04-FEB-1993; 93US-00014082.
XX PR 22-SEP-1993; 93US-00125462.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Rybak SM, Newton DL, Nicholls PJ, Youle RJ;
XX
XX WPI; 1999-560488/47.
XX
XX Recombinantly fused pancreatic RNase-targeting proteins useful for
XX treating tumors, infections, immune or autoimmune disorders and as a
XX contraceptive.
XX
XX Example 3; Fig 19; 47pp; English.
XX
XX This invention describes a novel nucleic acid construct comprising
XX sequences encoding functional pancreatic RNase and a second protein
XX (preferably the light and heavy chains of an antibody) which binds a
XX specific cell surface marker on a target cell and functions as a
XX cytotoxic agent. The products can be used for selectively killing cells
XX expressing a specific surface marker. They can be used for treating
XX tumors or infected cells (e.g. cells infected by viruses (especially
XX latent or chronic virus infections, such as human immunodeficiency virus
XX (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and
XX II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster,
XX cytomegalovirus)) and cells infected with parasites (such as the malaria
XX parasite)). They can also be used for treating immune dysfunctional cells
XX in immune and autoimmune diseases. Additionally, they may be used as
XX contraceptives. Finally they can also be used for cell separation in
XX vitro by selectively killing unwanted types of cells (e.g. in bone
XX marrow) prior to transplantation into a patient undergoing marrow
XX ablation by radiation or for killing leukemia cells or T-cells that would
XX cause graft-versus-host disease. This sequence represents a bullfrog

Query Match 99.2%; Score 602; DB 2; Length 111;
 Best Local Similarity 99.1%; Pred. No. 6.2e-61;
 Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGNWATFOQKHIIINTPIICNTIMDNNIYIVGGQCKRVNTFISSATTVKAICTGVINNV 60
 DB 1 MSNWATFOQKHIIINTPIICNTIMDNNIYIVGGQCKRVNTFISSATTVKAICTGVINNV 60

QY 61 LSTTRFQNTCTRTSITPRCPYSRSTETNYICVKENQYVPHFAGIGRCP 111
 DB 61 LSTTRFQNTCTRTSITPRCPYSRSTETNYICVKENQYVPHFAGIGRCP 111

RESULT 4
 AAY28876
 ID AAY28876 standard; protein; 111 AA.
 AC AAY28876;
 XX
 DT 25-JAN-2000 (first entry)
 DE Recombinant Met (-1) RaCOR1 Met22Leu Met57Leu- (His)6 protein.
 KW Met (-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu- (His)6; RaCOR1;
 KW recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
 KW cancer; bullfrog; RNase; autoimmune disease.
 XX Rana catesbeiana.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"
 FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"
 FT Misc-difference 23 /note= "Wild type Met replaced with Leu"
 FT Misc-difference 58 /note= "Wild type Met replaced with Leu"
 XX
 FN WO9950398-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 26-MAR-1999; 99WO-US006641.
 XX
 PR 27-MAR-1998; 98US-0079751P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Rybak SM, Newton DL;
 XX
 DR WPI; 1999-610847/52.
 XX
 DR N-PSDB; AAZ08133.
 XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.
 XX
 PS Claim 22; Page 66; 71pp; English.
 XX
 CC The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6
 CC tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant RaCOR1
 CC has a covalently bound ligand binding moiety, which can be a LL2 antibody
 CC directed against CD22 on cancerous B cells or human chorionic
 CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
 CC ribonucleases can be expressed in bacteria without an N-terminal
 CC methionine due to the presence of a signal peptide that is cleaved by
 CC bacteria. The soluble expression of ribonuclease allows the proteins to
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion

CC proteins. They can be used for treatment of cancer and autoimmune
 CC diseases
 XX
 SQ Sequence 111 AA;
 Query Match 99.0%; Score 601; DB 2; Length 111;
 Best Local Similarity 98.2%; Pred. No. 8.1e-61;
 Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNWATFOQKHIIINTPIICNTIMDNNIYIVGGQCKRVNTFISSATTVKAICTGVINNV 60
 DB 1 MGNWATFOQKHIIINTPIICNTILNDNIYIVGGQCKRVNTFISSATTVKAICTGVINLV 60

QY 61 LSTTRFQNTCTRTSITPRCPYSRSTETNYICVKENQYVPHFAGIGRCP 111
 DB 61 LSTTRFQNTCTRTSITPRCPYSRSTETNYICVKENQYVPHFAGIGRCP 111

RESULT 5
 AAY28877
 ID AAY28877 standard; protein; 110 AA.
 AC AAY28877;
 XX
 DT 25-JAN-2000 (first entry)
 DE Recombinant RaCOR1 Gln1Ser amino acid sequence.
 KW Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase;
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
 KW cancer; autoimmune disease.
 XX Rana catesbeiana.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"
 FT
 XX
 FN WO9950398-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 26-MAR-1999; 99WO-US006641.
 XX
 PR 27-MAR-1998; 98US-0079751P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Rybak SM, Newton DL;
 XX
 DR WPI; 1999-610847/52.
 XX
 DR N-PSDB; AAZ08133.
 XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.
 XX
 PS Claim 22; Page 67; 71pp; English.
 XX
 CC The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Gln1Ser. Carboxy terminal end of
 CC recombinant RaCOR1 has a covalently bound ligand binding moiety, which
 CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
 CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
 CC Recombinant ribonucleases can be expressed in bacteria without an N-
 CC terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases
 XX

CC cells. Recombinant ribonucleases can be expressed in bacteria without an
 CC N-terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases

XX SQ Sequence 111 AA;
 Query Match 100.0%; Score 607; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.7e-61;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQWATFQQRKHINTPIICNTIMDNNIYVGGQCKRVNTFIISATVKAICTGVINNV 60
 DB 1 MQWATFQQRKHINTPIICNTIMDNNIYVGGQCKRVNTFIISATVKAICTGVINNV 60

QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 111
 DB 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 111

RESULT 2
 AAY28872
 ID AAY28872 standard; protein; 110 AA.
 AC AAY28872;
 XX 25-JAN-2000 (first entry)
 DE Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.
 KW Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;
 KW LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;
 KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog;
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
 KW RNase.
 XX Rana catesbeiana.
 OS Synthetic.
 XX WO9950398-A2.
 XX 07-OCT-1999.
 XX 26-MAR-1999; 99WO-US006641.
 XX 27-MAR-1998; 98US-0079751P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Rybak SM, Newton DL;
 XX WPI; 1999-610847/52.
 XX N-PSDB; AAZ08130.
 XX New recombinant ribonucleases, used for killing target cells, e.g. for
 XX treating cancers, viral infections or autoimmune diseases.
 XX Claim 22; Page 62; 71pp; English.
 XX The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)
 XX protein encoded by a cDNA modified for expression in E. coli. Carboxy
 XX terminal end of RaCOR1 has a covalently bound ligand binding moiety,
 XX which can be a LL2 antibody directed against CD22 on cancerous B cells or
 XX human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma
 XX cells. Recombinant ribonucleases can be expressed in bacteria without an
 XX N-terminal methionine due to the presence of a signal peptide that is
 XX cleaved by bacteria. The soluble expression of ribonuclease allows the
 XX proteins to be fused in-frame with ligand binding moieties to form
 XX cytotoxic fusion proteins. They can be used for treatment of cancer and
 XX autoimmune diseases

SQ Sequence 110 AA;
 Query Match 99.2%; Score 602; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 6.1e-61;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNWATFQQRKHINTPIICNTIMDNNIYVGGQCKRVNTFIISATVKAICTGVINNV 61
 DB 1 QNWATFQQRKHINTPIICNTIMDNNIYVGGQCKRVNTFIISATVKAICTGVINNV 60

QY 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 111
 DB 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 110

RESULT 3
 AAY28878
 ID AAY28878 standard; protein; 111 AA.
 AC AAY28878;
 XX 25-JAN-2000 (first entry)
 DE Recombinant Met (-1) RaCOR1 Gln1Ser amino acid sequence.
 KW Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
 KW CD22; RNase; autoimmune disease.
 XX Rana catesbeiana.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"
 FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"
 XX WO9950398-A2.
 XX 07-OCT-1999.
 XX 26-MAR-1999; 99WO-US006641.
 XX 27-MAR-1998; 98US-0079751P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Rybak SM, Newton DL;
 XX WPI; 1999-610847/52.
 XX N-PSDB; AAZ08135.
 XX New recombinant ribonucleases, used for killing target cells, e.g. for
 XX treating cancers, viral infections or autoimmune diseases.
 XX Claim 22; Page 68; 71pp; English.
 XX The present sequence is a recombinant Rana catesbeiana ribonuclease
 XX (RaCOR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end
 XX of recombinant RaCOR1 has a covalently bound ligand binding moiety, which
 XX can be a LL2 antibody directed against CD22 on cancerous B cells or human
 XX chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
 XX Recombinant ribonucleases can be expressed in bacteria without an N-
 XX terminal methionine due to the presence of a signal peptide that is
 XX cleaved by bacteria. The soluble expression of ribonuclease allows the
 XX proteins to be fused in-frame with ligand binding moieties to form
 XX cytotoxic fusion proteins. They can be used for treatment of cancer and
 XX autoimmune diseases

XX SQ Sequence 111 AA;

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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:25:55 ; Search time 47.3489 Seconds
(without alignments)
662.376 Million cell updates/sec

Title: US-09-961-400-17
Perfect score: 607
Sequence: 1 MQNWATFOQKHIIPTICN.....ICVKCNQYFVFAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep_29Jan04.*
1: Genesep1980s.*
2: Genesep1990s.*
3: Genesep2000s.*
4: Genesep2001s.*
5: Genesep2002s.*
6: Genesep2003as.*
7: Genesep2003bs.*
8: Genesep2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	607	100.0	111	2	AAY28873 Recombina
2	602	99.2	110	2	AAY28872 Rana cate
3	602	99.2	111	2	AAY28878 Recombina
4	601	99.0	111	2	AAY28876 Recombina
5	597	98.4	110	2	AAY28877 Recombina
6	596	98.2	110	2	AAY28874 Recombina
7	588.5	97.0	111	2	AAY33321 Frog lect
8	286.5	47.2	105	2	AAY28867 Recombina
9	284.5	46.9	104	2	AAY28867 Recombina
10	283.5	46.7	105	2	AAY28869 Recombina
11	282.5	46.5	105	2	AAY39400 Recombina
12	281.5	46.4	104	2	AAY28865
13	281.5	46.4	105	2	AAY28871 Recombina
14	281.5	46.4	127	2	AAY28879 Rana pipi
15	279.5	46.0	105	2	AAY35123 R. pipien
16	279.5	46.0	355	2	AAY35125 R. pipien
17	279.5	46.0	358	2	AAY35130 R. pipien
18	278.5	45.9	104	2	AAY28866 Recombina
19	277.5	45.7	104	2	AAY30301 Recombina
20	277.5	45.7	104	2	AAB31666 Amino aci
21	277.5	45.7	104	5	ABG32650 Northern
22	277.5	45.7	112	2	ABG32650 Northern
23	277.5	45.7	251	2	AAY35118 R. pipien
24	277.5	45.7	254	2	AAY35134 R. pipien
25	277.5	45.7	355	2	AAY35135 R. pipien
26	277.5	45.7	355	2	AAY35133 R. pipien

26	277.5	45.7	355	2	AAW35129	R. pipien
27	277.5	45.7	366	2	AAW35132	R. pipien
28	277.5	45.7	379	2	AAW35126	R. pipien
29	276.5	45.6	104	2	AAY28870	Recombina
30	274.5	45.2	104	2	AAW12344	Protein w
31	274.5	45.2	104	2	AAW47303	ONCONASE
32	274.5	45.2	104	2	AAW00736	Protein d
33	274.5	45.2	104	2	AAW14065	Onconase
34	274.5	45.2	104	2	AAW06543	Antitumou
35	274.5	45.2	104	2	AAW88233	Rana pipi
36	274.5	45.2	104	2	AAY33322	Frog onco
37	272.5	44.9	104	4	ABG31667	Amino aci
38	272.5	44.9	104	5	ABG31617	Northern
39	272.5	44.9	105	2	AAW35116	R. pipien
40	272.5	44.9	106	2	AAW35122	R. pipien
41	272.5	44.9	107	2	AAW35117	R. pipien
42	271.5	44.7	104	2	AAW30302	Recombina
43	271.5	44.7	105	2	AAW35115	R. pipien
44	268.5	44.2	358	2	AAW35127	R. pipien
45	268.5	44.2	365	2	AAW35131	R. pipien

ALIGNMENTS

RESULT 1

AAY28873
ID AAY28873 standard; protein; 111 AA.

XX AC AAY28873;

XX 25-JAN-2000 (first entry)

XX Recombinant Met (-1) RaCOR1.

XX Recombinant Met (-1) RaCOR1.

KW Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;
covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
KX recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
KW RNase; autoimmune disease.

XX Rana catesbeiana.
OS Synthetic.

XX Rana catesbeiana.

PH Key Location/Qualifiers

FT Misc-difference 1

FT /note= "Met not found in wild type RaCOR1"

XX WO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US0006641.

XX 27-MAR-1998; 98US-0079751P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;

XX WPI; 1999-610847/52.

XX N-PSDB; AA208131.

XX New recombinant ribonucleases, used for killing target cells, e.g. for
treating cancers, viral infections or autoimmune diseases.

XX Claim 22; Page 63; 71pp; English.

XX The present sequence is a recombinant Rana catesbeiana oocyte
ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal

CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
which can be a LL2 antibody directed against CD22 on cancerous B cells, or
human chorionic gonadotropin (hCG) effective against Kaposi's sarcoma


```

RN      SEQUENCE OF 31-114 FROM N.A.
RP      MEDLINE=93367815; PubMed=8360916;
RX      Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P.,
RA      Carsana A., Palmieri M., Furia A.;
RA      "sequences related to the ox pancreatic ribonuclease coding region in
RT      the genomic DNA of mammalian species.";
RL      J. Mol. Evol. 37:29-35(1993).
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
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EMBL; S81743; AAB36137.1; -.
EMBL; S65126; AAB27931.1; -.
DR      HSPSP; P00656; 2RNS.
DR      InterPro; IPR001427; RNaseA.
DR      Pfam; PF00074; rnaaseA; 1.
DR      PRINTS; PR00794; RIBONUCLEASE.
DR      ProDom; PD000535; RNaseA; 1.
DR      SMART; SM00092; RNase_Pc; 1.
DR      PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW      Hydrolase; Nuclease; Endonuclease; glycoprotein.
FT      ACT_SITE 41
FT      DISULFID 26 84
FT      DISULFID 40 95
FT      DISULFID 58 110
FT      DISULFID 65 72
FT      CARBOHYD 62 62
FT      CARBOHYD 129 129
FT      SEQUENCE 141 AA; 15592 MW; 73745E9F979591F CRC64;
-----
QY      4  ATFOOKHI-----INTPLICNTMDNNIYIVGGCKRVNTFISSATTVAICTGVINM 57
DB      6  AKFREQHMDSGSSSSSNYNQNMKRR-RMTHGCKPNTFVHESLADVAVCS---QK 61
QY      58 NVL-----SITREQLNCTCTTSITPRP-CFYSSRTETNYTCVKE-NOY_PVHFA 104
DB      62 NITCKNGQPCVQSNTWNITDCRETSKYPNCAYKTSQKQYITVACEGNYFYPVHFD 121
QY      105 G 105
DB      122 G 122
-----
RESULT 15
RNBR AXIPR
ID      RNBR AXIPR      STANDARD;      PRT;      151 AA.
AC      P87350;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN      BRN.
OS      Axis porcinus (Hog deer).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC      Cervidae; Cervinae; Axis.
OX      NCBI_TaxID=57737;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98278842; PubMed=9611269;
RA      Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,

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SQ SEQUENCE 124 AA; 13804 MW; 0AC28CDE14111845 CRC64;

Query Match
Best Local Similarity 22.0%; Score 132.5; DB 1; Length 124;
Matches 36; Conservative 19; Mismatches 42; Indels 17; Gaps 6;

QY 6 FQOKHI-----INTPIIONTMNNIYVGQCKRVNTFTFISSATTVKAICTGV-INNM 58
Db ||::|| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
8 FORQMOPDSSSNSNYSNCLMMRR-NWTGCRCKPVTNVFHSLSADVQAVCSQINVCX 66
QY 59 VLSTTRFOLNT-----CTRISITPRP-CPYSSRTEINYICVKENQ--YPVHF 103
Db ||::|| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
67 NGQTNCYQSNSPMHTIDCRGTGGSSKYPCAYKASQEQKHIVACEGNPPVPVHF 120

RESULT 11
RNP_IGUIG STANDARD; PRT; 119 AA.
AC P80287;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.1.27.5) (RNase 1) (RNase A).
OS Iguna iguana (Common iguana).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX NCBI_TaxID=8517;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=94139745; PubMed=8307028;
RA Zhao W., Beintema J.J., Hofsteenge J.;
RT "The amino acid sequence of iguana (Iguana iguana) pancreatic
ribonuclease.";
RL Eur. J. Biochem. 219:641-646(1994).
CC -|- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3',-phosphooligonucleotides ending in C-P or U-P
with 2',3',-cyclic phosphate intermediates.
-|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Pancreas.
CC -|- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PRS; S41111; S41111.
DR HSP; P00656; IL5Q.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; ENDO nuclease; Pyrididone carboxylic acid.
FT DISULFID 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT FT 25 80 BY SIMILARITY.
FT FT 39 91 BY SIMILARITY.
FT FT 57 106 BY SIMILARITY.
FT FT 10 10 BY SIMILARITY.
FT ACT_SITE 40 40 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.
SQ SEQUENCE 119 AA; 13324 MW; 6072FB5B7B15BD5A CRC64;

Query Match
Best Local Similarity 21.8%; Score 131.5; DB 1; Length 119;
Matches 35; Conservative 16; Mismatches 51; Indels 13; Gaps 4;

QY 1 QNWATFQQKHI-----INTPIICWTTMNNIYVGQCKRVNTFTFISSATTVKAIC-- 51
Db ||::|| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
1 QDWSSFNKHIDYPTFSASNPNAYCDLWMQR-NLNPTKCTRYTFVHASESEIQCVGS 59
QY 52 --TGVINMVLTSTRPOLNTCTRTSIT-PRCPYSSRTEETNYICKVENQYPVHF 103
Db ||::|| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
60 GGTHVEDNLYDNESFDLTDCKNVGGTAPSSCKYNGTGTKRIACENNQPVHF 114

RESULT 12

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16-OCT-2001 (Rel. 40, Last annotation update)
RN. Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9203604; PubMed=1754384;
RA Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,
RA Viola M., Palmieri M., Russo E., Furia A.;
RT "Molecular cloning of the gene encoding the bovine brain ribonuclease
and its expression in different regions of the brain."
RL Nucleic Acids Res. 19:6469-6474 (1991).
RN [2]
RP SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.
RC TISSUE=Brain;
RX MEDLINE=89214015; PubMed=3243767;
RA Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,
RA Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bovine brain."
RL J. Biochem. 104:939-945 (1988).
RN [3]
RP SEQUENCE OF 27-167 FROM N.A.
RX MEDLINE=96139017; PubMed=8587129;
RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA Vento M.T., Furia A.;
RT "Molecular evolution of genes encoding ribonucleases in ruminant
species."
RL J. Mol. Evol. 41:850-858 (1995).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@sb-sib.ch).
CC -----
EMBL; X59767; CAA2439.1; -;
EMBL; S81744; AAB36138.1; -;
PIR; S20066; S20066.
HSP; P00656; 2RNS.
GlycoSuiteDB; P39873; -;
InterPro; IPR001427; RNaseA.
Pfam; PF00074; RNaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00032; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR Hydroxylase; Nuclease; Endonuclease; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 167 RIBONUCLEASE, BRAIN.
FT ACT_SITE 38 38 BY SIMILARITY.
FT ACT_SITE 67 67 BY SIMILARITY.
FT ACT_SITE 145 145 BY SIMILARITY.
FT DISULFID 52 110 BY SIMILARITY.
FT DISULFID 66 121 BY SIMILARITY.
FT DISULFID 84 136 BY SIMILARITY.
FT DISULFID 91 98 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .).
FT CARBOHYD 155 155 O-LINKED.
FT CARBOHYD 159 159 O-LINKED.
FT CONFLICT 155 155 T -> S (IN REF. 2).
SQ SEQUENCE 167 AA; 18450 MW; 681CAAC3CC2FC459 CRC64;
Query Match 22.2%; Score 133.5; DB 1; Length 167;
Best Local Similarity 31.4%; Pred. No. 2.2e-07;

Matches 38; Conservative 17; Mismatches 43; Indels 23; Gaps 7;
QY 4 ATEQOKHI-----INTPIICNTMDNNIYIVGGCKRVNTFIISATTVAICTGVINM 57
DB 32 AKFRQHQHDSGSSSSNNYCNQMKRR-RMTHGCKPNTFVHESLDDVKAACS--QK 87
QY 58 NVL-----STTFQLNTCTRTSTTPRP-CPYSSRTETNYICVKE-NQY-PVHFA 104
DB 88 NITCKNGHPCVQSKSTMSITDCRETGSGKYPNCAYKTSQKQYITVACEGPNYPVPHF 147
QY 105 G 105
DB 148 G 148
RESULT 10
RNP_PIG STANDARD; PRT; 124 AA.
ID AC P00671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=70104197; PubMed=5460946;
RA Jackson R.L., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. II. The
amino acid sequence of the reduced S-aminoethylated protein."
RL J. Biol. Chem. 245:637-653 (1970).
RN [2]
RP REVISION TO 2.
RA Wierenga R.K., Huizinga J.D., Gastra W., Welling G.W., Beintema J.J.;
RT "Affinity chromatography of porcine pancreatic ribonuclease and
reinvestigation of the N-terminal amino acid sequence."
RL FEBS Lett. 31:181-185 (1973).
RN [3]
RP DISULFIDE BONDS.
RX MEDLINE=70104198; PubMed=4904878;
RA Phelan J.J., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. 3. The
disulfide bonds."
RL J. Biol. Chem. 245:654-661 (1970).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Pancreas.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PIR; A92071; NREG.
HSP; P00656; 1SRN.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; RNaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00032; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR Hydroxylase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84
FT DISULFID 40 95
FT DISULFID 58 110
FT DISULFID 65 72
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .).
FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .).

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DR PTR; A00818; NRWHK.
DR HSP; P00656; LSRN.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNaseA; 1.
KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 76 76 N-LINKED (GLCNAC...) (30%).
SQ SEQUENCE 124 AA; 14125 MW; 57475459F697E20 CRC64;

Query Match 22.5%; Score 135.5; DB 1; Length 124;
Best Local Similarity 33.3%; Pred. No. 9.7e-08;
Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

QY 6 EQQKHII-----NTPLICNTIMNNIYVGGCKRVNTFIISATVTKAICTGVINMV 59
Db 8 FQOHMDSGNSPGNNPNYCNQMMRR--KMTQGRCKPVNTFVHESLEDVKAVCS---QKNV 63
QY 60 L-----STTRFQNTCTRTSITPR-CPYSSSTNTNYICVKE-NQY-PVHF 103
Db 64 LCKNGRTNCYESNSTWHITDCTGSKYPNCAKTSQKEKHIVACEGNNPYVPVHF 120

RESULT 8
ANGI_MOUSE
ID ANGI_MOUSE STANDARD; PRT; 145 AA.
AC P21570;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91025023; PubMed=2222458;
RA Bond M.D., Vallee B.L.;
RA "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Rata S.S., Loquellano N.A., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra N.A.;
RT "Generation and initial analysis of more than 15,000 full-length

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human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP PARTIAL SEQUENCE.
RC TISSUE=Serum;
RX MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
angiogenins: discernment of functionally important residues and
regions.";
RL Biochim. Biophys. Acta 1162:177-186(1993).
CC -!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
to actin on the surface of endothelial cells; once bound,
angiogenin is endocytosed and translocated to the nucleus, thereby
promoting the endothelial invasiveness necessary for blood vessel
formation. Angiogenin induces vascularization of normal and
malignant tissues. Abolishes protein synthesis by specifically
hydrolyzing cellular tRNAs.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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CC EMBL; U22516; AAA91366.1; -.
DR EMBL; BC055355; AH55355.1; -.
DR PIR; A35932; A35932.
DR HSP; P03950; 1A4Y.
DR MGD; MGI:88022; Ang.
DR InterPro; IPR001427; RNaseA.
DR PRINTS; PR00074; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNaseA; 1.
KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 145 ANGIOENIN.
FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (BY
SIMILARITY).
FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT ACT_SITE 137 137 BY SIMILARITY.
FT DISULFID 50 104 BY SIMILARITY.
FT DISULFID 63 115 BY SIMILARITY.
FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA; 16228 MW; 06944260B764938 CRC64;

Query Match 22.5%; Score 135.5; DB 1; Length 145;
Best Local Similarity 39.5%; Pred. No. 1.1e-07;
Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3;

QY 33 CKRVNTFIISATVTKAIC---TGVINMV-LSTTRFQNTCTRTSITPR-PCPYSSRTE 87
Db 63 CKDVTFTHGKSNKAIKANGSPYRENRMSKSPFQVTTCKTGGSPRPPCQYRASAG 122
QY 88 TNYICVKENQYVPVHF 103
Db 123 FRHVVVIACENGLPVHF 138

RESULT 9
RNER_BOVIN
ID RNER_BOVIN STANDARD; PRT; 167 AA.
AC P39873;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)

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CC residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C)
CC as substrates, and prefers the former. The S-lectins in frog eggs
CC may be involved in the fertilization and development of the frog
CC embryo. This lectin agglutinates various animal cells, including
CC normal lymphocytes, erythrocytes, and fibroblasts of animal and
CC human origin. It is cytotoxic against several tumor cells.
CC
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AF039104; AAD10702.1; -.
CC PIR; A27121; A27121.
CC PDB; 1BC4; 28-OCT-98.
CC PDB; 1M07; 21-JAN-03.
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; RNaseA; 1.
CC ProDom; PD000535; RNaseA; 1.
CC SMART; SM00092; RNaseA; 1.
CC PROSITE; PS00127; RNASE PANCREATIC; 1.
CC KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
CC Signal; Pyrrolidone carboxylic acid.
CC
CC SIGNAL 1 22
CC CHAIN 23 133 RIBONUCLEASE, OOCYTES.
CC FT MOD RES 23 23 PYRROLIDONE CARBOXYLIC ACID.
CC FT ACT SITE 32 32
CC FT ACT_SITE 57 57
CC FT ACT_SITE 125 125
CC FT ACT_SITE 125 125
CC FT DISULFID 41 93
CC FT DISULFID 56 103
CC FT DISULFID 74 118
CC FT DISULFID 115 132
CC FT HELIX 25 32
CC FT HELIX 41 45
CC FT TURN 48 49
CC FT STRAND 59 63
CC FT HELIX 67 73
CC FT TURN 74 74
CC FT STRAND 79 84
CC FT STRAND 90 95
CC FT STRAND 105 110
CC FT STRAND 114 119
CC FT TURN 120 121
CC FT STRAND 122 129
CC SQ SEQUENCE 133 AA; A7D62594F7D16F0C CRC64;
CC
CC Query Match 98.3%; Score 591.5; DB 1; Length 133;
CC Best Local Similarity 99.1%; Pred. No. 1.1e-56;
CC Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
CC
CC QY 1 QNWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMV 59
CC Db 23 QNWATFOQKHINTPIINCNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMV 82
CC
CC QY 60 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGRCP 110
CC Db 83 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGRCP 133
CC
CC RESULT 2
CC LECS_RANJA
CC ID LECS_RANJA STANDARD; PRT; 111 AA.
CC AC P18839;
CC DT 01-NOV-1990 (Rel. 16, Created)
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)

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DE Sialic acid-binding lectin (EC 3.1.1.27.-).
OS Rana japonica (Japanese reddish frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Egg;
RX MEDLINE=91035319; PubMed=2229005;
RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
RA Takayanagi Y., Iitani K.;
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT eggs."
RL J. Biochem. 108:139-143(1990).
CC -!- FUNCTION: The S-lectins in frog eggs may be involved in the
CC fertilization and development of the frog embryo. This lectin
CC preferentially agglutinates a large variety of tumor cells, but it
CC does not agglutinate non-transformed cells and erythrocytes.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC PIR; JX0120; JX0120.
DR HSP; P11916; IBC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
DR KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin;
KW Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT SITE 10 10
FT ACT_SITE 35 35
FT ACT_SITE 104 104
FT DISULFID 19 72
FT DISULFID 34 82
FT DISULFID 52 97
FT DISULFID 94 111
FT SQ SEQUENCE 111 AA; 12326 MW; FDBBDDF3834ED679 CRC64;
CC
CC Query Match 75.6%; Score 455; DB 1; Length 111;
CC Best Local Similarity 78.4%; Pred. No. 4.1e-42;
CC Matches 87; Conservative 7; Mismatches 15; Indels 2; Gaps 2;
CC
CC QY 1 QNWATFOQKHINTP-IICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGV-INNV 58
CC Db 1 QNWAKFQEKHIPNTSINCNTIMDKSIYVGGQCKRVNTFISSATTVKAICSGASTRN 60
CC
CC QY 59 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGRCP 109
CC Db 61 VLSTTRFQNLNCTRTSITPRPCPYNSRTETNYICVKENRLPVHFAGIGRCP 111
CC
CC RESULT 3
CC RNPL_RANJA
CC ID RNPL_RANJA STANDARD; PRT; 111 AA.
CC AC P14626;
CC DT 01-APR-1990 (Rel. 14, Created)
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Ribonuclease, liver (EC 3.1.1.27.5).
CC OS Rana catesbeiana (Bull frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=90130374; PubMed=2613682;
RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
RA Okazaki T., Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
RT liver."

```

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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:30:40 ; Search time 5.55659 Seconds

(without alignments)
1030.796 Million cell updates/sec

Title: US-09-961-400-15

Perfect score: 602

Sequence: 1 QNWATFOOKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	591.5	98.3	133	1	RNPO_RANCA
2	455	75.6	111	1	LECS_RANJA
3	374	62.1	111	1	RNPL_RANCA
4	277.5	46.1	104	1	RN30_RANPI
5	154.5	25.7	145	1	ANG3_MOUSE
6	149.5	24.8	145	1	ANGR_MOUSE
7	135.5	22.5	124	1	RNP_BALAC
8	135.5	22.5	145	1	ANGI_MOUSE
9	132.5	22.0	167	1	RNBR_BOVIN
10	132.5	22.0	124	1	RNP_PIG
11	131.5	21.8	119	1	RNP_IGUIG
12	128.5	21.3	151	1	RNBR_CAPCA
13	127.5	21.2	123	1	ANG2_BOVIN
14	127.5	21.2	141	1	RNBR_GIRCA
15	127.5	21.2	151	1	RNBR_AXIPR
16	125	20.8	146	1	ANGI_SAIAC
17	124	20.6	146	1	ANGI_MIOTA
18	123.5	20.5	143	1	RNBR_SHEEP
19	122.5	20.3	124	1	RNP_ANTAM
20	122.5	20.3	146	1	ANGI_CERAE
21	122	20.3	122	1	RNP_MACRU
22	120.5	20.0	128	1	RNP_MYOOC
23	120.5	20.0	149	1	RNP_MOUSE
24	120	19.9	146	1	ANGI_AOTTR
25	120	19.9	147	1	ANGI_PONPY
26	119.5	19.9	123	1	ANGI_PIG
27	118.5	19.7	128	1	RNBR_CAVIO
28	118	19.6	146	1	ANGI_SAGOE
29	117.5	19.5	128	1	RNP_HORSE
30	116.5	19.4	124	1	RNP_CAMDR
31	116.5	19.4	128	1	RNP_PROGU
32	115.5	19.2	119	1	RNS4_BOVIN
33	115.5	19.2	146	1	ANGI_MACMU

34	114	18.9	148	1	ANGI_BOVIN
35	113.5	18.9	124	1	RNP_RANTA
36	113.5	18.9	146	1	ANGI_PAPHA
37	113	18.8	147	1	ANGI_HUMAN
38	113	18.8	147	1	ANGI_PANTR
39	112.5	18.7	124	1	RNP_CAPCA
40	112.5	18.7	124	1	RNP_GIRCA
41	112.5	18.7	148	1	RNS4_MOUSE
42	112	18.6	125	1	ANGI_RABIT
43	111.5	18.5	130	1	ANGI_CRILLO
44	111.5	18.5	147	1	RNS4_RAT
45	111.5	18.5	149	1	RNP_ACOCA

ALIGNMENTS

RESULT 1
RNPO_RANCA STANDARD; PRT; 133 AA.
AC P11916; Q9PWR7;
DT 01-OCT-1989 (Rel. 12, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).
DE binding lectin)
GN RCR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98165825; PubMed=9497370;
RA Huang H.C., Wang S.C., Lu Y.J., Lu S.C., Liao Y.D.;
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease. Tissue distribution, cloning, purification, cytotoxicity, and active residues for RNase activity.";
RT J. Biol. Chem. 273:6395-6401(1998).
RL [2]
RP SEQUENCE OF 23-133.
RX TISSUE=Egg;
RA MEDLINE=87299649; PubMed=3304421;
RA Titani K.; Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H., Takayanagi G., Hakomori S.;
RT "Amino acid sequence of sialic acid binding lectin from frog (Rana catesbeiana) eggs.";
RL Biochemistry 26:2189-2194(1987).
RN [3]
RP CHARACTERIZATION, AND SEQUENCE OF 81-101.
RX MEDLINE=9220613; PubMed=1373237;
RA Liao Y.-D.;
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana catesbeiana (bullfrog) oocytes.";
RL Nucleic Acids Res. 20:1371-1377(1992).
RN [4]
RP CHARACTERIZATION.
RC TISSUE=Egg;
RX MEDLINE=93192604; PubMed=8448385;
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H., Takayanagi Y., Hakomori S., Titani K.;
RT "Ribonuclease activity of sialic acid-binding lectin from Rana catesbeiana eggs.";
RL Glycobiology 3:37-45(1993).
RN [5]
RP STRUCTURE BY NMR OF 23-133.
RX MEDLINE=98437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
RT "The solution structure of a cytotoxic ribonuclease from the oocytes of Rana catesbeiana (bullfrog).";
RL J. Mol. Biol. 283:231-244(1998).
CC -!- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine

```
QY 33 CKENVTFIISATVKAICTG-----VINNVLTSTRFQNTCTRTSITPR-PCPYSSRTE 87
Db 39 CKENVTFIHGTRNDIKAIKNDKNGEPYNNFRSKSPFQITTCXKKGSGNRPCCGYRATAG 98
QY 88 TNYICVKCENQYFVHF 103
Db 99 FRTIACENGLPVHF 114

RESULT 15
NRGPB
pancreatic ribonuclease (EC 3.1.1.27.5) B - guinea pig (tentative sequence)
N;Alternate names: RNase IB
C;Species: Cavia porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
R;van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gastra, W.; Beintema, J.J.
Eur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a
A;Reference number: A91247; MUID:77185023; PMID:862624
A;Accession: A00826
A;Molecule type: protein
A;Residues: 1-128 <VAN>
A;Note: 64-pro was also found
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein, hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match 19, 7%; Score 118.5; DB 1; Length 128;
Best Local Similarity 31.6%; Pred. No. 8.5e-05;
Matches 37; Conservative 14; Mismatches 43; Indels 23; Gaps 6;

QY 6 FQQRHI-----INTPIICNTIMDNIIYVGGQCKRVNTFIISATVKAICTGVINNV 59
Db 8 FQRQMDPEGSPSSNVCNVMITRR-NMTQGRCKPVNTFVHESLADYQAVC---FQKNV 63

QY 60 L-----STTRFQNTCTRTSITPR-CPYSSRTETNYICVKCENQ--YFVHF 103
Db 64 LCKNGQTNICYQSYGRMRITDCRVTSSTSSKFPNCNCRMSQAKSIIVACEGDPYFVHF 120
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Search completed: May 7, 2004, 21:54:55
Job time : 10.9813 secs


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Db 6 AKFERQHIDSNPSSVSSNYCNQMMKSR-NLTQGRCKPVNTFFVHESLADVQAVCS---QK 61
QY 58 NVL-----STTRFQLNCTRTSITPRP-CPYSSRTEINVCVKE-NOY-PVHF 103
Db 62 NVACKNGQTCYQSYSTMSITDCRETGSSKYPENCAKTKTQAKKHIIIVACEGNFPVPVHY 120

RESULT 11
NRKGR
pancreatic ribonuclease (EC 3.1.1.27.5) - red kangaroo
N;Alternate names: RNase A
C;Species: Macropus rufus, Megaleia rufa (red kangaroo)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C;Accession: A00833
R;Gaastera, W.; Welling, G.W.; Beintema, J.J.
Eur. J. Biochem. 86, 209-217, 1978
A;Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A;Reference number: A00833; MUID:78190621; PMID:658039
A;Accession: A00833
A;Molecule type: protein
A;Residues: 1-122 <GAA>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;11,40,117/Active site: His, Lys, His #status predicted
F;25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
F;61/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 20.3%; Score 122; DB 1; Length 122;
Best Local Similarity 30.7%; Pred. No. 3.6e-05;
Matches 35; Conservative 16; Mismatches 45; Indels 18; Gaps 6;

QY 6 FQOKHI-----INTPLICNTIMNNIYVGGCKRVNTFISSATTVKAIC----- 51
Db 7 FQOHMDTHTSHASSSNYCNLMKAR-DMTSGCKPLNTFIHPKSVDAVCHQENVTCK 65

QY 52 TGVNNVLSTTRFQLNCTRTSITPRP-CPYSSRTEINVCVKE-NOY-PVHF 103
Db 66 NGRINC-YKSNLSLITNCRGASKYPCQVETSNLNQLIIVACEGQVVPVHF 118

RESULT 12
NRUC
pancreatic ribonuclease (EC 3.1.1.27.5) - nutria (tentative sequence)
N;Alternate names: RNase A
C;Species: Myocastor coypus (nutria, coypu)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Accession: A00822
R;van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A;Reference number: A90612; MUID:77065676; PMID:999896
A;Accession: A00822
A;Molecule type: protein
A;Residues: 1-128 <VAN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;13,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 20.0%; Score 120.5; DB 1; Length 128;
Best Local Similarity 31.6%; Pred. No. 5.4e-05;
Matches 37; Conservative 15; Mismatches 42; Indels 23; Gaps 7;

QY 6 FQOKHI-----INTPLICNTIMNNIYVGGCKRVNTFISSATTVKAICTGVINNV 59
Db 8 FERQHMDSRGSPSTNPYCNEMKSR-NMTQGRCKPVNTFFVHEPLADVQAVC---FQKNV 63

QY 60 L-----STTRFQLNCTRTSITPRP-CPYSSRTEINVCVKE-NOY-PVHF 103
Db 64 LCKNGQTCYQSYSTMSITDCRETGSSKYPENCAKTKTQAKKHIIIVACEGNFPVPVHF 120
```

RESULT 13

NRMS

```
pancreatic ribonuclease (EC 3.1.1.27.5) precursor - mouse
N;Alternate names: RNase A
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C;Accession: A34090; S22598; A00830
R;Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
Mol. Biol. Evol. 7, 29-44, 1990
A;Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse
A;Reference number: A34090; MUID:90136034; PMID:2299980
A;Accession: A34090
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-149 <SCH>
A;Cross-references: GB:M27814; NID:g200762; PIDN:AAA40060.1; PID:g200763
R;Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.
Nucleic Acids Res. 19, 6935-6941, 1991
A;Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific
A;Reference number: S22598; MUID:92107684; PMID:1840677
A;Accession: S22598
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <SAM>
A;Cross-references: EMBL:X60103; NID:g53981; PIDN:CRA42697.1; PID:g53982
R;Lenstra, J.A.; Beintema, J.J.
Eur. J. Biochem. 98, 399-408, 1979
A;Title: The amino acid sequence of mouse pancreatic ribonuclease.
A;Reference number: A00830; MUID:80024269; PMID:556267
A;Accession: A00830
A;Molecule type: protein
A;Residues: 26-149 <LEN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-149/Product: pancreatic ribonuclease #status experimental <MAT>
F;37,66,144/Active site: His, Lys, His #status predicted
F;51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted
F;62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.0%; Score 120.5; DB 1; Length 149;
Best Local Similarity 30.8%; Pred. No. 6.3e-05;
Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;

QY 6 FQOKHI-----INTPLICNTIMNNIYVGGCKRVNTFISSATTVKAICTGVINNV 59
Db 33 FQOHMDPDGSGINSPTYCNQMKRR-DMTSGCKPNTFFVHEPLADVQAVCS---QENV 88

QY 60 L-----STTRFQLNCTRTSITPRP-CPYSSRTEINVCVKE-NOY-PVHF 103
Db 89 TCKNRKSNCKYSSSALHTDCHLKNSKYPENCDYKTKTQYQKHIIIVACEGNFPVPVHF 145

RESULT 14
A43825
angiotensin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S29834; A43825
R;Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A;Title: Characterization and sequencing of rabbit, pig and mouse angiotensins: discernme
A;Reference number: S29833; MUID:93192291; PMID:8448182
A;Accession: S29834
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-123 <BN>
A;Note: this sequence was submitted to the Protein Sequence Database, December 1992
C;Superfamily: pancreatic ribonuclease

Query Match 19.9%; Score 119.5; DB 1; Length 123;
Best Local Similarity 39.5%; Pred. No. 6.5e-05;
Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;
```

RESULT 8
BNRPG
pancreatic ribonuclease (EC 3.1.27.5) - pig
;Alternate names: RNase A
;Species: Sus scrofa domestica (domestic pig)
;Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text_change 03-Jun-1994
;Accession: A92071; A91391; A00816
;Jackson, R.L.; Hirs, C.H.W.
;Biol. Chem. 245, 637-653, 1970
;Title: The primary structure of porcine pancreatic ribonuclease. II. The amino acid
;Reference number: A92071; MUID: 70104197; PMID: 5460946
;Accession: A92071
;Molecule type: protein
;Residues: 1,'Q',3-124 <JAC>
;Wieringa, R.K.; Huizinga, J.D.; Gaastra, W.; Welling, G.W.; Beintema, J.J.
;FEBS Lett. 31, 181-185, 1973
;Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation
;Reference number: A91391
;Accession: A91391
;Molecule type: protein
;Residues: 1-124 <WIE>
;Phelan, J.J.; Hirs, C.H.W.
;Biol. Chem. 245, 654-661, 1970
;Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide bond
;Reference number: A92072; MUID: 70104198; PMID: 4904878
;Contents: annotation; disulfide bonds
;Supersfamily: pancreatic ribonuclease

[illegible]

QY 1 QNWATFOQKHINTP-IICNTIMDNNIYVGGCKRVNTFIISATTVKAICTGV-INNN 58
 Db 1 QNWAKFOEKHPNTSNINCNTIMDKSIYVGGCKERTNTFIISATTVKAICSGASTRN 60

QY 59 VLSTTRFQMLNCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRC 109
 Db 61 VLSTTRFQMLNCTRSATAPPCPNSTETNYICVKCENRLPVHFAGIGRC 111

RESULT 3
 JX0085
 C:Species: Rana catesbeiana (bullfrog)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
 C:Accession: JX0085
 R:Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg
 J. Biochem. 106, 729-735, 1989
 A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
 A:Reference number: JX0085; MUID:90130374; PMID:2613682
 A:Accession: JX0085
 A:Molecule type: protein
 A:Residues: 1-111 <NIT>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: hydrolase; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:10.35,104/Active site: His, Lys, His #status predicted
 F:19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted

Query Match 62.1%; Score 374; DB 2; Length 111;
 Best Local Similarity 65.8%; Pred. No. 2.9e-30;
 Matches 73; Conservative 27; Mismatches 27; Indels 2; Gaps 2;

QY 1 QNWATFOQKHINTPII-ONTIMDNNIYVGGCKRVNTFIISATTVKAICTGVI-NMN 58
 Db 1 QNWAKFEKHRTSSIDCNTIMDKAIYVGGCKERTNTFIISDENVKAICSGVSPDRK 60

QY 59 VLSTTRFQMLNCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRC 109
 Db 61 ELSTTSFKLNTCIRDSITPRPCPYSPDNNKICVCKEQLPVHFGVIGKC 111

RESULT 4
 A39035
 C:Species: Rana pipiens (northern leopard frog)
 C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
 C:Accession: A39035
 R:Ardelt, W.; Mikulski, S.M.; Shogen, K.
 J. Biol. Chem. 266, 245-251, 1991
 A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl
 A:Reference number: A39035; MUID:91093131; PMID:1985896
 A:Accession: A39035
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-104 <ARD>
 C:Superfamily: pancreatic ribonuclease

Query Match 45.6%; Score 274.5; DB 2; Length 104;
 Best Local Similarity 48.6%; Pred. No. 2.1e-20;
 Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGCKRVNTFIISATTVKAICTGVI-NMN 58
 Db 1 EDWTFQKHHTNRDVCDDNIMSTNLF----HCKDKNTIYSRPEPVKAICKGLIASKN 56

QY 59 VLSTTRFQMLNCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRC 109
 Db 57 VLITSEYLSDC---NVTSEPKYKLSKSTNKFCVTCENQAPVHFVGVGSC 104

RESULT 5
 NRWHK
 C:Species: Rana pipiens (northern leopard frog)
 C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
 C:Accession: A39035
 R:Ardelt, W.; Mikulski, S.M.; Shogen, K.
 J. Biol. Chem. 266, 245-251, 1991
 A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl
 A:Reference number: A39035; MUID:91093131; PMID:1985896
 A:Accession: A39035
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-104 <ARD>
 C:Superfamily: pancreatic ribonuclease

N;Alternate names: RNase 1; RNase A
 C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
 C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
 C:Accession: A00818
 R;Emmens, M.; Welling, G.W.; Beintema, J.J.
 Biochem. J. 157, 317-323, 1976
 A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
 A:Reference number: A00818; MUID:76277855; PMID:962870
 A:Accession: A00818
 A:Molecule type: protein
 A:Residues: 1-124 <EMM>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:12.41,113/Active site: His, Lys, His #status predicted
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
 F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 22.5%; Score 135.5; DB 1; Length 124;
 Best Local Similarity 33.3%; Pred. No. 1.7e-06;
 Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

QY 6 FQOKHII-----NPIICNTIMDNNIYVGGCKRVNTFIISATTVKAICTGVINNV 59
 Db 8 FQOFMDSGNSPGNNPNYCNQMMER-KMTQGRCKPVNTFVHESLEDVKAVCS---QKNV 63

QY 60 L-----STTRFQMLNCTRTSITPRP-CPYSSRTETNYICVKE-NQY-PVHF 103
 Db 64 LCKNGRTNCEBSNTMHTDCROTGSSKYPNCAYKTSQKXKHIIVACEGNYVPVHF 120

RESULT 6
 A35932
 C:Species: Mus musculus (house mouse)
 C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
 C:Accession: A35932
 R;Bond, M.D.; Vallee, B.L.
 Biochem. Biophys. Res. Commun. 171, 988-995, 1990
 A:Title: Isolation and sequencing of mouse angiogenin DNA.
 A:Reference number: A35932; MUID:91025023; PMID:222458
 A:Accession: A35932
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-145 <BON>
 A:Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326
 C:Genetics: #status absent
 C:Function:
 A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-145/Product: angiogenin #status predicted <MAT>
 F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
 F:37,64,137/Active site: His, Lys, His #status predicted
 F:50-104,63-115,81-130/Disulfide bonds: #status predicted

Query Match 22.5%; Score 135.5; DB 1; Length 145;
 Best Local Similarity 39.5%; Pred. No. 2e-06;
 Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3;

QY 33 CKRVNTFIISATTVKAIC---TGVINNV-ISTTRFQMLNCTRTSITPR-PCPYSSRTE 87
 Db 63 CKDVTNFIHGKSNKAICGANGSPYRENLRMSKSPFQVTTCKTGTSRPPCQYRASAG 122

QY 88 TNVICKCNQYVPHF 103
 Db 123 FRHWIACENGLEVFHF 138

RESULT 7

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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:38:36 ; Search time 9.98129 Seconds
(without alignments)
1060.090 Million cell updates/sec

Title: US-09-961-400-15
Perfect score: 602
Sequence: 1 QNWATFOQKHINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*

1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	588.5	97.8	111	2 A27121	ribonuclease-relat
2	455	75.6	111	1 JX0120	ribonuclease-relat
3	374	62.1	111	2 JX0085	pancreatic ribonuc
4	274.5	45.6	104	2 A39035	ribonuclease-relat
5	135.5	22.5	124	1 NRWHK	pancreatic ribonuc
6	135.5	22.5	145	1 A35932	angiogenin precurs
7	133.5	22.2	167	2 S20066	pancreatic-type ri
8	132.5	22.0	124	1 NRPG	pancreatic ribonuc
9	131.5	21.8	119	2 S41111	pancreatic ribonuc
10	122.5	20.3	124	1 NRPRH	pancreatic ribonuc
11	122	20.3	122	1 NRKGR	pancreatic ribonuc
12	120.5	20.0	128	1 NRCU	pancreatic ribonuc
13	120.5	20.0	149	1 NRMS	pancreatic ribonuc
14	119.5	19.9	123	1 A43825	pancreatic ribonuc
15	118.5	19.7	128	1 NRGPB	pancreatic ribonuc
16	117.5	19.5	128	1 NRHO	pancreatic ribonuc
17	116.5	19.4	124	1 NRCM	pancreatic ribonuc
18	116.5	19.4	124	1 NRCMM	pancreatic ribonuc
19	116.5	19.4	124	1 NRCMB	pancreatic ribonuc
20	116.5	19.4	128	1 NRKS	pancreatic ribonuc
21	114.5	19.0	124	2 S08549	ribonuclease - dom
22	114	18.9	125	1 A32474	angiogenin [valida
23	113.5	18.9	124	1 NRDEN	pancreatic ribonuc
24	113	18.8	147	1 NRHUAG	angiogenin precurs
25	112.5	18.7	124	1 NRGF	pancreatic ribonuc
26	112.5	18.7	124	1 NRDEO	pancreatic ribonuc
27	112	18.6	125	1 B43825	angiogenin - rabbi
28	111.5	18.5	130	2 S22808	pancreatic ribonuc
29	110.5	18.4	124	1 NRBOB	pancreatic ribonuc

30 110.5 18.4 124 1 NRWB pancreatic ribonuc

31 110.5 18.4 124 1 NREKN pancreatic ribonuc

32 110.5 18.4 124 2 S07141 pancreatic ribonuc

33 110.5 18.4 150 1 NRBO pancreatic ribonuc

34 110.5 18.4 158 2 I61900 eosinophil-derived

35 109.5 18.2 124 1 NRSH pancreatic ribonuc

36 108.5 18.0 119 2 JX0115 pancreatic ribonuc

37 108.5 18.0 124 1 NRCS pancreatic ribonuc

38 108.5 18.0 152 1 NRRT pancreatic ribonuc

39 106.5 17.7 124 1 NRHP pancreatic ribonuc

40 106.5 17.7 125 4 A47498 seminal ribonuclea

41 106.5 17.7 150 1 NRBOB seminal ribonuclea

42 104.5 17.4 124 1 NRGN pancreatic ribonuc

43 104.5 17.4 124 1 NRDEF pancreatic ribonuc

44 104 17.3 125 2 S04503 pancreatic ribonuc

45 103.5 17.2 124 2 S08546 pancreatic ribonuc

ALIGNMENTS

RESULT 1

A27121
ribonuclease-related sialic acid-binding lectin - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
R:Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayanagi
Biochemistry 26, 2189-2194, 1987
A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A:Reference number: A27121; MUID:87299649; PMID:3304421
A:Accession: A27121
A:Molecule type: protein
A:Residues: 1-111 <TIT>
C:Superfamily: pancreatic ribonuclease
C:Keywords: lectin

Query Match 97.8%; Score 588.5; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 1.4e-51;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Qy 1 QNWATFOQKHINTPII-CNTIMDNNTIYVGQCKRVNTFISSATTVKAICTGVNNV 59
Db 1 ENWATFOQKHINTPII-CNTIMDNNTIYVGQCKRVNTFISSATTVKAICTGVNNV 60
Qy 60 LSTTRFQNTCTRTSITPRCPYSSRTETNVICVKCENQYPVHFAGIGRCP 110
Db 61 LSTTRFQNTCTRTSITPRCPYSSRTETNVICVKCENQYPVHFAGIGRCP 111

RESULT 2

JX0120

ribonuclease-related sialic acid-binding lectin - Japanese frog
C:Species: Rana japonica (Japanese frog)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R:Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takayanagi
J. Biochem. 108, 139-143, 1990
A:Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.
A:Reference number: JX0120; MUID:91035319; PMID:2229005
A:Accession: JX0120

A:Molecule type: protein
A:Residues: 1-111 <KAM>
A:Experimental source: egg
C:Superfamily: pancreatic ribonuclease
C:Keywords: lectin; pyrrolidone carboxylic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:19-72,34-82,52-97,94-111/Dsulfide bonds: #status experimental

Query Match 75.6%; Score 455; DB 1; Length 111;
Best Local Similarity 78.4%; Pred. No. 2.6e-38;
Matches 87; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

NAME/KEY: Protein
 LOCATION: 1..104
 OTHER INFORMATION: /label= Onc
 OTHER INFORMATION: /note= "Onconase from Rana pipiens"
 US-08-891-848-13

Query Match 45.6%; Score 274.5; DB 2; Length 104;
 Best Local Similarity 48.6%; Pred. No. 1.7e-24;
 Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTMDNNIYVGGCKRVNTFISSATTVAICTGVI-NNN 58
 Db 1 EDWLTFOQKHINTTRDVCDCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 56
 QY 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
 Db 57 VLTTFSEFYLSDC--NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 104

RESULT 14

US-08-875-811-39
 Sequence 39, Application US/08875811
 Patent No. 6045793

GENERAL INFORMATION:
 APPLICANT: Rybak, Susanna M.
 APPLICANT: Newton, Dianne L.
 APPLICANT: Boque, Lluís
 APPLICANT: Wlodawer, Alexander
 TITLE OF INVENTION: Recombinant Ribonuclease Proteins
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/875,811
 FILING DATE: 19-FEB-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/02588
 FILING DATE: 19-FEB-1997

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/011,800
 FILING DATE: 21-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Faris, Susan K.
 REGISTRATION NUMBER: 41,739
 REFERENCE/DOCKET NUMBER: 015280-244100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 105 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-875-811-39

Query Match 45.6%; Score 274.5; DB 3; Length 105;
 Best Local Similarity 48.6%; Pred. No. 1.7e-24;
 Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTMDNNIYVGGCKRVNTFISSATTVAICTGVI-NNN 58
 Db 1 EDWLTFOQKHINTTRDVCDCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 56

Db 2 EDWLTFOQKHINTTRDVCDCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 57
 QY 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
 Db 58 VLTTFSEFYLSDC--NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 105

RESULT 15

US-08-875-811-41
 Sequence 41, Application US/08875811
 Patent No. 6045793

GENERAL INFORMATION:
 APPLICANT: Rybak, Susanna M.
 APPLICANT: Newton, Dianne L.
 APPLICANT: Boque, Lluís
 APPLICANT: Wlodawer, Alexander
 TITLE OF INVENTION: Recombinant Ribonuclease Proteins
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/875,811
 FILING DATE: 19-FEB-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/02588
 FILING DATE: 19-FEB-1997

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/011,800
 FILING DATE: 21-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Faris, Susan K.
 REGISTRATION NUMBER: 41,739
 REFERENCE/DOCKET NUMBER: 015280-244100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 41:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 355 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-875-811-41

Query Match 45.6%; Score 274.5; DB 3; Length 355;
 Best Local Similarity 48.6%; Pred. No. 7.7e-24;
 Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTMDNNIYVGGCKRVNTFISSATTVAICTGVI-NNN 58
 Db 252 EDWLTFOQKHINTTRDVCDCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 307
 QY 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
 Db 308 VLTTFSEFYLSDC--NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 355

Search completed: May 7, 2004, 21:40:45
 Job time : 13.7596 secs


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/ ANTI-SENSE: N
/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/ ORGANISM: Rana pipiens
/ DEVELOPMENTAL STAGE: Embryo
US-07-921-619-1

Query Match 45.6%; Score 274.5; DB 1; Length 104;
Best Local Similarity 48.6%; Pred. No. 1.7e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVI-NMN 58
Db 1 EDWLTFOQKHINTRDVDCDNIIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

QY 59 VLSITTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 57 VLTTFSEFYLSDC---NVTSRPFCKYKLKXSTNKFVCVTCEQAQVHFVGVGSC 104

RESULT 12
US-08-467-955-1
/ Sequence 1, Application US/08467955
/ Patent No. 5728805
/ GENERAL INFORMATION:
/ APPLICANT: Ardelt Ph.D. Wojciech J.
/ TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Mark H. Jay, P.A.
/ STREET: P.O. Box E
/ CITY: Short Hills
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07078-0383
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.24
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/467,955
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/178,118
/ FILING DATE: 06-APR-1988
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/436,141
/ FILING DATE: 13-NOV-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/814,332
/ FILING DATE: 03-FEB-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/283,970
/ FILING DATE: 01-AUG-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jay, Mark H.
/ REGISTRATION NUMBER: 27507
/ REFERENCE/DOCKET NUMBER: 5007 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-912-9066
/ TELEFAX: 201-912-0442
/ TELEX: No. 5728805 Applicable
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 104 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: N
/ ANTI-SENSE: N

/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/ ORGANISM: Rana pipiens
/ DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-1

Query Match 45.6%; Score 274.5; DB 1; Length 104;
Best Local Similarity 48.6%; Pred. No. 1.7e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVI-NMN 58
Db 1 EDWLTFOQKHINTRDVDCDNIIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

QY 59 VLSITTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 57 VLTTFSEFYLSDC---NVTSRPFCKYKLKXSTNKFVCVTCEQAQVHFVGVGSC 104

RESULT 13
US-08-891-848-13
/ Sequence 13, Application US/08891848
/ Patent No. 5955073
/ GENERAL INFORMATION:
/ APPLICANT: Rybak, Susanna M.
/ APPLICANT: Youle, Richard J.
/ APPLICANT: Newton, Dianne L.
/ APPLICANT: Nicholls, Peter J.
/ TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
/ NUMBER OF SEQUENCES: 19
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/891,848
/ FILING DATE: No. 5955073 yet assigned
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/125,462
/ FILING DATE: 22-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/014,082
/ FILING DATE: 04-FEB-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/779,195
/ FILING DATE: 22-OCT-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/510,696
/ FILING DATE: 20-APR-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Weber, Ellen Lauver
/ REGISTRATION NUMBER: 32,762
/ REFERENCE/DOCKET NUMBER: 015280-110310US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 104 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
```

APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-43

Query Match 46.1%; Score 277.5; DB 3; Length 379;
Best Local Similarity 49.5%; Pred. No. 3.7e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNVIVGQCKRVNTFISSATTVKAICTGVI-NMN 58
DB 26 QDWLTFQKKHINTRDVDCDNIMSNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 81
QY 59 VLSTTRFOLNCTRTSITPRPCPYSSRTETNYICVKCNQXVPVHFAGIGRC 109
DB 82 VLTTFSEFYLSDC---NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 129

RESULT 10
US-08-283-971-1
Sequence 1, Application US/08283971
Patent No. 5529775
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D. Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,971
FILING DATE: 06-APR-1988
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/921,180
FILING DATE: 30-JUL-1992
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5006 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
TELEFAX: 718-625-0399
TELEX: No. 5529775 Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 104 amino acids
TYPE: amino acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
US-08-283-971-1

Query Match 45.6%; Score 274.5; DB 1; Length 104;
Best Local Similarity 48.6%; Pred. No. 1.7e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNVIVGQCKRVNTFISSATTVKAICTGVI-NMN 58
DB 1 EDWLTFFQKKHINTRDVDCDNIMSNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 56
QY 59 VLSTTRFOLNCTRTSITPRPCPYSSRTETNYICVKCNQXVPVHFAGIGRC 109
DB 57 VLTTFSEFYLSDC---NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 104

RESULT 11
US-07-921-619-1
Sequence 1, Application US/07921619
Patent No. 5595734
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D. Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,619
FILING DATE: 19920728
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5005 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
TELEFAX: 718-625-0399
TELEX: No. 5595734 Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: AMINO ACID
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: N

```

/ APPLICANT: Wu, Yon-Neng
/ APPLICANT: Boix, Ester
/ APPLICANT: Argelt, Wojciech
/ TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
/ TITLE OF INVENTION: Allows Production by Recombinant Methods
/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew
/ STREET: One Market Plaza, Steuart Street Tower
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94105-1492
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/095,429
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/626,288
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ran, David B.
/ REGISTRATION NUMBER: 38,589
/ REFERENCE/DOCKET NUMBER: 15280-267
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 543-9600
/ TELEFAX: (415) 543-5043
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 104 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-09-095-429-1
/
/ Query March 46.1%; Score 277.5; DB 4; Length 104;
/ Best Local Similarity 49.5%; Pred. No. 7.7e-25;
/ Matches 55; Conservative 15; Mismatches 32; Indels 9
/
/ Qy 1 QNWATPFOQKHINT-PIICNTIMDNNIYVGGCKRYNTFIISATTVKALC
/ Db 1 QDWLTFQKHGHINTRDVDCNIMSTNLF---HCKDKNTIYSRPEPVKALC
/
/ Qy 59 VLSTTRFQNLCTRTSITPRPCYSRSRTETNYICVKCENQYPVHFAGIGRC
/ Db 57 VLTTSEFYLSDC--NVTSRPCKYKLLKSTNKFCVTENQAPVHFVGVGSC
/
/ RESULT 8
/ US-08-875-811-63
/ Sequence 63, Application US/08875811
/ Patent No. 6045793
/ GENERAL INFORMATION:
/ APPLICANT: Rybak, Susanna M.
/ APPLICANT: Newton, Dianne L.
/ APPLICANT: Boque, Lluís
/ APPLICANT: Wlodawer, Alexander
/ TITLE OF INVENTION: Recombinant Ribonuclease Proteins
/ NUMBER OF SEQUENCES: 64
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:

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1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFISSATTVKAICTGVI-NMN 58

RESULT 7
US-09-095-429-1
; Sequence 1, Application US/09095429
; Patent No. 6649393
; GENERAL INFORMATION:
; APPLICANT: Youle, Richard
; APPLICANT: Vasandani, Vena

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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
; OTHER INFORMATION: /note= "Frog Lectin from Rana
; catesbeiana"
US-08-891-848-12

Query Match 97.8%; Score 588.5; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 7.4e-61;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 QNWATFOQKHLINPTII-CNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNV 59
Db 1 ENWATFOQKHLINPTIINCNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNV 60

Qy 60 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 2
US-08-875-811-8
; Sequence 8, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111

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; OTHER INFORMATION: /note= "Frog Lectin from Rana
; catesbeiana"
US-08-875-811-8

Query Match 97.8%; Score 588.5; DB 3; Length 111;
Best Local Similarity 98.2%; Pred. No. 7.4e-61;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 QNWATFOQKHLINPTII-CNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNV 59
Db 1 ENWATFOQKHLINPTIINCNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNV 60

Qy 60 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D, Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; TELEX: No. 5728805 Applicable
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:28:45 ; Search time 12.7596 Seconds
(without alignments)
445.066 Million cell updates/sec

Title: US-09-961-400-15
Perfect score: 602
Sequence: 1 QNWFQKHIINTPIICNT.....ICVKCNQYPVHPAGRCGP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625371 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	588.5	97.8	111	2	US-08-891-848-12
2	588.5	97.8	111	3	US-08-875-811-8
3	284.5	47.3	104	1	US-08-467-955-2
4	277.5	46.1	104	3	US-09-394-268-1
5	277.5	46.1	104	4	US-09-687-748-1
6	277.5	46.1	104	4	US-08-626-288-1
7	277.5	46.1	104	4	US-09-095-429-1
8	277.5	46.1	129	3	US-08-875-811-63
9	277.5	46.1	379	3	US-08-875-811-43
10	274.5	45.6	104	1	US-08-283-971-1
11	274.5	45.6	104	1	US-07-921-619-1
12	274.5	45.6	104	1	US-08-467-955-1
13	274.5	45.6	104	2	US-08-891-848-13
14	274.5	45.6	105	3	US-08-875-811-39
15	274.5	45.6	355	3	US-08-875-811-41
16	274.5	45.6	358	3	US-08-875-811-51
17	272.5	45.3	104	3	US-08-875-811-1
18	272.5	45.3	104	4	US-09-394-268-2
19	272.5	45.3	104	4	US-09-071-672-1
20	272.5	45.3	104	4	US-09-687-748-2
21	272.5	45.3	104	4	US-09-966-119-1
22	272.5	45.3	106	3	US-08-875-811-28
23	272.5	45.3	107	3	US-08-875-811-30
24	272.5	45.3	112	3	US-08-875-811-32
25	272.5	45.3	251	3	US-08-875-811-59
26	272.5	45.3	254	3	US-08-875-811-61
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28 272.5 45.3 355 3 US-08-875-811-57
29 272.5 45.3 355 3 US-08-875-811-64
30 272.5 45.3 366 3 US-08-875-811-55
31 269.5 44.8 104 4 US-08-626-288-2
32 269.5 44.8 104 4 US-09-095-429-2
33 267.5 44.4 105 3 US-08-875-811-24
34 267.5 44.4 105 3 US-08-875-811-26
35 263.5 43.8 358 3 US-08-875-811-45
36 263.5 43.8 365 3 US-08-875-811-53
37 249.5 41.4 107 3 US-08-875-811-20
38 239.5 39.8 111 3 US-08-875-811-22
39 236 39.2 114 3 US-09-223-118-3
40 227.5 37.8 360 3 US-08-875-811-47
41 227 37.7 114 3 US-09-223-118-2
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ALIGNMENTS

RESULT 1
US-08-891-848-12
; Sequence 12 Application US/08891848
; Patent No. 5955073
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Youle, Richard J.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Nicholls, Peter J.
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,848
; FILING DATE: No. 5955073 yet assigned
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,462
; FILING DATE: 22-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/014,082
; FILING DATE: 04-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,195
; FILING DATE: 22-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/510,696
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-110310US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid


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CC (Rana catesbeiana) lectin used to describe the method of the invention
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SQ Sequence 111 AA;

Query Match          97.8%; Score 588.5; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 2.2e-59;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 QNWATFOCKHINTPII-CNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINNV 59
Db 1 ENWATFOCKHINTPIINCNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINNV 60

Qy 60 LSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 61 LSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 8
AAW06544
ID AAW06544 standard; protein; 104 AA.
XX
AC AAW06544;
XX
DI 22-AUG-1997 (first entry)
XX
DE Antitumour protein from Rana pipiens oocytes.
XX
KW Tumour; chemotherapy; radiotherapy; frog.
XX
OS Rana pipiens.
XX
PN W09639428-A1.
XX
PD 12-DEC-1996.
XX
PF 03-JUN-1996; 96WO-US008304.
XX
PR 06-JUN-1995; 95US-00467955.
XX
PA (ALFA-) ALFACELL CORP.
XX
FI Ardelt WJ;
XX
DR WPI; 1997-043063/04.
XX
PT Antitumour proteins from Rana pipiens oocyte(s) - have fewer
PT disadvantages than chemotherapy, surgery and radiotherapy.
XX
PS Claim 8; Page 28; 45pp; English.
XX

The present sequence is a specifically claimed example of an antitumour
protein from the generic protein in AAW18224, with the molecular weight
CC 12000. This is one of two preferred proteins (the other in AAW06543) that
CC have been isolated from Rana pipiens oocytes. Both proteins have a
CC blocked amino terminal group and are essentially free of carbohydrates.
CC The proteins are used to treat tumours. Use of the peptides has fewer
CC disadvantages than chemotherapy, radiotherapy and surgery in the
CC treatment of tumours
XX
SQ Sequence 104 AA;

Query Match          47.3%; Score 284.5; DB 2; Length 104;
Best Local Similarity 49.5%; Pred. No. 1.3e-24;
Matches 55; Conservative 16; Mismatches 31; Indels 9; Gaps 4;

Qy 1 QNWATFOCKHINT-PIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVI 58
Db 1 EDWLTFOCKHVTNRDVCNNIMTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

Qy 59 VLSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 57 VLTTSEFYLSDC---NVTSRCKYKLLKSKNTFCVTCENQAPVHFVGVRG 104

CC (Rana catesbeiana) lectin used to describe the method of the invention
XX
SQ Sequence 111 AA;

Query Match          97.8%; Score 588.5; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 2.2e-59;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 QNWATFOCKHINTPII-CNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINNV 59
Db 1 ENWATFOCKHINTPIINCNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINNV 60

Qy 60 LSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 61 LSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 8
AAW06544
ID AAW06544 standard; protein; 104 AA.
XX
AC AAW06544;
XX
DI 22-AUG-1997 (first entry)
XX
DE Antitumour protein from Rana pipiens oocytes.
XX
KW Tumour; chemotherapy; radiotherapy; frog.
XX
OS Rana pipiens.
XX
PN W09639428-A1.
XX
PD 12-DEC-1996.
XX
PF 03-JUN-1996; 96WO-US008304.
XX
PR 06-JUN-1995; 95US-00467955.
XX
PA (ALFA-) ALFACELL CORP.
XX
FI Ardelt WJ;
XX
DR WPI; 1997-043063/04.
XX
PT Antitumour proteins from Rana pipiens oocyte(s) - have fewer
PT disadvantages than chemotherapy, surgery and radiotherapy.
XX
PS Claim 8; Page 28; 45pp; English.
XX

The present sequence is a specifically claimed example of an antitumour
protein from the generic protein in AAW18224, with the molecular weight
CC 12000. This is one of two preferred proteins (the other in AAW06543) that
CC have been isolated from Rana pipiens oocytes. Both proteins have a
CC blocked amino terminal group and are essentially free of carbohydrates.
CC The proteins are used to treat tumours. Use of the peptides has fewer
CC disadvantages than chemotherapy, radiotherapy and surgery in the
CC treatment of tumours
XX
SQ Sequence 104 AA;

Query Match          47.3%; Score 284.5; DB 2; Length 104;
Best Local Similarity 49.5%; Pred. No. 1.3e-24;
Matches 55; Conservative 16; Mismatches 31; Indels 9; Gaps 4;

Qy 1 QNWATFOCKHINT-PIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVI 58
Db 1 EDWLTFOCKHVTNRDVCNNIMTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

Qy 59 VLSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 57 VLTTSEFYLSDC---NVTSRCKYKLLKSKNTFCVTCENQAPVHFVGVRG 104
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RESULT 9
AAZ28865
ID AAZ28865 standard; protein; 104 AA.
XX
AC AAZ28865;
XX
DT 25-JAN-2000 (first entry)
XX
DE Rana pipiens liver ribonuclease (RaPLR1).
XX
KW Rana pipiens liver ribonuclease; RaPLR1; covalently bound; LL2 antibody;
KW ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog;
KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase;
KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
XX
OS Rana pipiens.
XX
PN W09950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
XX
N-PSDB; AAZ08124.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 1; Page 55; 71pp; English.
XX

The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein.
Carboxy terminal end of RaPLR1 has a covalently bound ligand binding
CC moiety, which can be a LL2 antibody directed against CD22 on cancerous B
CC cells or human chorionic gonadotrophin (hCG) effective against Kaposi's
CC Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria
CC without an N-terminal methionine due to the presence of a signal peptide
CC that is cleaved by bacteria. The soluble expression of ribonuclease
CC allows the proteins to be fused in-frame with ligand binding moieties to
CC form cytotoxic fusion proteins. They can be used for treatment of cancer
CC and autoimmune diseases
XX
SQ Sequence 104 AA;

Query Match          46.8%; Score 281.5; DB 2; Length 104;
Best Local Similarity 49.5%; Pred. No. 2.9e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFOCKHINT-PIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVI-NMN 58
Db 1 QDWLTFOCKHVTNRDVCNNIMTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

Qy 59 VLSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 57 VLTTSEFYLSDC---NVTSRCKYKLLKSKNTFCVTCENQAPVHFVGVRG 104

RESULT 10
AAZ28867
ID AAZ28867 standard; protein; 105 AA.
XX
AC AAZ28867;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant Met (-1) RaPLR1.
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QY 1 QNWATFOQKHIIINPIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVINLNV 60
Db 1 QNWATFOQKHIIINPIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVINLNV 60
QY 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 6
AA228876
ID AAY28876 standard; protein; 111 AA.
XX
AC AAY28876;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant Met (-1) RacOR1 Met22Leu Met57Leu- (His)6 protein.
XX
KW Met (-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu- (His)6; RacOR1;
KW recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;
KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;
KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW cancer; bullfrog; RNase; autoimmune disease.
XX
OS Rana catesbeiana.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Met not found in wild type RacOR1"
FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"
FT Misc-difference 23 /note= "Wild type Met replaced with Leu"
FT Misc-difference 58 /note= "Wild type Met replaced with Leu"
XX
XX WO9950398-A2.
XX
XX 07-OCT-1999.
XX
XX 26-MAR-1999; 99WO-US006641.
XX
XX 27-MAR-1998; 98US-0079751P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
XX WPI; 1999-610847/52.
XX
XX N-PSDB; AAZ08133.
XX
XX New recombinant ribonucleases, used for killing target cells, e.g. for
XX treating cancers, viral infections or autoimmune diseases.
XX
XX Claim 22; Page 66; 71pp; English.
XX
XX The present sequence is a recombinant Rana catesbeiana oocyte
XX ribonuclease (RacOR1) protein with Met at position 1 attached to a (His)6
XX tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant RacOR1
XX has a covalently bound ligand binding moiety, which can be a LL2 antibody
XX directed against CD22 on cancerous B cells or human chorionic
XX gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant
XX ribonucleases can be expressed in bacteria without an N-terminal
XX methionine due to the presence of a signal peptide that is cleaved by
XX bacteria. The soluble expression of ribonuclease allows the proteins to
XX be fused in-frame with ligand binding moieties to form cytotoxic fusion
XX proteins. They can be used for treatment of cancer and autoimmune
XX diseases
XX
XX Sequence 111 AA;

```

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Query Match 99.0%; Score 596; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 3e-60; Indels 0; Gaps 0;
Matches 108; Conservative 2; Mismatches 0;

QY 1 QNWATFOQKHIIINPIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVINLNV 60
Db 2 QNWATFOQKHIIINPIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVINLNV 61

QY 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 7
AA233321
ID AAY33321 standard; protein; 111 AA.
XX
AC AAY33321;
XX
DT 29-NOV-1999 (first entry)
XX
DE Frog lectin protein fragment.
XX
KW Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;
KW heavy chain; cell surface marker; treatment; tumor; viral infection;
KW parasite infection; immune dysfunctional cell; autoimmune disease;
KW contraceptive; cell separation; transplantation; bone marrow ablation;
KW leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
XX
OS Rana catesbeiana.
XX
XX US9555073-A.
XX
XX 21-SEP-1999.
XX
XX 09-JUL-1997; 97US-00891848.
XX
XX 20-APR-1990; 90US-00510696.
XX
XX 22-OCT-1991; 91US-00779195.
XX
XX 04-FEB-1993; 93US-00014082.
XX
XX 22-SEP-1993; 93US-00125462.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Rybak SM, Newton DL, Nicholls PJ, Youle RJ;
XX
XX WPI; 1999-560488/47.
XX
XX Recombinantly fused pancreatic RNase-targeting proteins useful for
XX treating tumors, infections, immune or autoimmune disorders and as a
XX contraceptive.
XX
XX Example 3; Fig 19; 47pp; English.
XX
XX This invention describes a novel nucleic acid construct comprising
XX sequences encoding functional pancreatic RNase and a second protein
XX (preferably the light and heavy chains of an antibody) which binds a
XX specific cell surface marker on a target cell and functions as a
XX cytotoxic agent. The products can be used for selectively killing cells
XX expressing a specific surface marker. They can be used for treating
XX tumors or infected cells (e.g. cells infected by viruses (especially
XX latent or chronic virus infections, such as human immunodeficiency virus
XX (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and
XX II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster,
XX cytomegalovirus) and cells infected with parasites (such as the malaria
XX parasite)). They can also be used for treating immune dysfunctional cells
XX in immune and autoimmune diseases. Additionally, they may be used as
XX contraceptives. Finally they can also be used for cell separation in
XX vitro by selectively killing unwanted types of cells (e.g. in bone
XX marrow) prior to transplantation into a patient undergoing marrow
XX ablation by radiation or for killing leukemia cells or T-cells that would
XX cause graft-versus-host disease. This sequence represents a bullfrog

```

Best Local Similarity 100.0%; Pred. No. 2.3e-60;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 2 NWATFOQKHINTPIICNTIMDNNTIYVGGQCKRVNTFIISATTVKAICTGVINNVLS 61
Db 2 NWATFOQKHINTPIICNTIMDNNTIYVGGQCKRVNTFIISATTVKAICTGVINNVLS 61
QY 62 TTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 62 TTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
```

RESULT 4

AAAY28878
ID AAY28878 standard; protein; 111 AA.

XX AC AAY28878;

XX DT 25-JAN-2000 (first entry)

XX DE Recombinant Met (-1) RaCOR1 Gln1Ser amino acid sequence.

KW Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1;
KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
KW CD22; RNase; autoimmune disease.

XX OS Rana catesbeiana.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"

XX FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"

XX FT WO9950398-A2.

XX PN 07-OCT-1999.

XX PD 26-MAR-1999; 99WO-US006641.

XX PF 27-MAR-1998; 98US-0079751P.

XX PR (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PA Rybak SM, Newton DL;

XX PI WPI; 1999-610847/52.

XX XX N-PSDB; AAZ08135.

XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
XX treating cancers, viral infections or autoimmune diseases.

XX PS Claim 22; Page 68; 71pp; English.

XX CC The present sequence is a recombinant Rana catesbeiana ribonuclease
XX (RaCOR1) protein with Met at position 1 and Gln28er. Carboxy terminal end
XX of recombinant RaCOR1 has a covalently bound ligand binding moiety, which
XX can be a LL2 antibody directed against CD22 on cancerous B cells or human
XX chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
XX Recombinant ribonucleases can be expressed in bacteria without an N-
XX terminal methionine due to the presence of a signal peptide that is
XX cleaved by bacteria. The soluble expression of ribonuclease allows the
XX proteins to be fused in-frame with ligand binding moieties to form
XX cytotoxic fusion proteins. They can be used for treatment of cancer and
XX autoimmune diseases

XX SQ Sequence 111 AA;

Query Match

Best Local Similarity 100.0%; Pred. No. 2.3e-60;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFOQKHINTPIICNTIMDNNTIYVGGQCKRVNTFIISATTVKAICTGVINNVLS 61

Db 3 NWATFOQKHINTPIICNTIMDNNTIYVGGQCKRVNTFIISATTVKAICTGVINNVLS 62

QY 62 TTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110

Db 63 TTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 5

AAAY28874
ID AAY28874 standard; protein; 110 AA.

XX AC AAY28874;

XX DT 25-JAN-2000 (first entry)

XX DE Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.

KW Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound;
KW RaCOR1 Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22;
KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW cancer; bullfrog; RNase; autoimmune disease.

XX OS Rana catesbeiana.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 22 /note= "Wild type Met replaced with Leu"

XX FT Misc-difference 57 /note= "Wild type Met replaced with Leu"

XX FT WO9950398-A2.

XX PN 07-OCT-1999.

XX PD 26-MAR-1999; 99WO-US006641.

XX PF 27-MAR-1998; 98US-0079751P.

XX PR (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PA Rybak SM, Newton DL;

XX PI WPI; 1999-610847/52.

XX XX N-PSDB; AAZ08132.

XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
XX treating cancers, viral infections or autoimmune diseases.

XX PS Claim 22; Page 64; 71pp; English.

XX CC The present sequence is a recombinant Rana catesbeiana oocyte
XX ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal
XX end of recombinant RaCOR1 has a covalently bound ligand binding moiety, or
XX which can be a LL2 antibody directed against CD22 on cancerous B cells or
XX human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
XX cells. Recombinant ribonucleases can be expressed in bacteria without an
XX N-terminal methionine due to the presence of a signal peptide that is
XX cleaved by bacteria. The soluble expression of ribonuclease allows the
XX proteins to be fused in-frame with ligand binding moieties to form
XX cytotoxic fusion proteins. They can be used for treatment of cancer and
XX autoimmune diseases

XX SQ Sequence 110 AA;

Query Match

Best Local Similarity 99.2%; Pred. No. 3e-60;

Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases

SQ Sequence 110 AA;

Query Match 100.0%; Score 602; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 6.1e-61;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNWATFOQKHIIINTPIICNTIMDNIIYVGGCKRVNTFISSATVKAICTGVINMNVL 60
 Db 1 QNWATFOQKHIIINTPIICNTIMDNIIYVGGCKRVNTFISSATVKAICTGVINMNVL 60

QY 61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGRCP 110
 Db 61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGRCP 110

RESULT 2
 AAY28873
 ID AAY28873 standard; protein; 111 AA.

AC AAY28873;
 XX 25-JAN-2000 (first entry)
 DT Recombinant Met (-1) RaCOR1.
 DE Recombinant Met (-1) RaCOR1.
 KW Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
 KW RNase; autoimmune disease.
 XX Rana catesbeiana.
 OS Synthetic.

Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"

XX WO9950398-A2.
 XX 07-OCT-1999.
 XX 26-MAR-1999; 99WO-US006641.
 XX 27-MAR-1998; 98US-0079751P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA Rybak SM, Newton DL;
 PI WPI; 1999-610847/52.
 DR N-PSDB; AAZ08131.
 XX New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.

XX Claim 22; Page 63; 71pp; English.

XX The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal
 CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or
 CC human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an
 CC N-terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases

SQ Sequence 111 AA;

Query Match 100.0%; Score 602; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6.2e-61;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNWATFOQKHIIINTPIICNTIMDNIIYVGGCKRVNTFISSATVKAICTGVINMNVL 60
 Db 2 QNWATFOQKHIIINTPIICNTIMDNIIYVGGCKRVNTFISSATVKAICTGVINMNVL 61

QY 61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGRCP 110
 Db 62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGRCP 111

RESULT 3
 AAY28877
 ID AAY28877 standard; protein; 110 AA.

AC AAY28877;
 XX 25-JAN-2000 (first entry)
 DT Recombinant RaCOR1 Gln1Ser amino acid sequence.

DE Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase;
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
 KW cancer; autoimmune disease.
 XX Rana catesbeiana.
 OS Synthetic.

Key Location/Qualifiers
 FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"

XX WO9950398-A2.
 XX 07-OCT-1999.
 XX 26-MAR-1999; 99WO-US006641.
 XX 27-MAR-1998; 98US-0079751P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA Rybak SM, Newton DL;
 PI WPI; 1999-610847/52.
 DR N-PSDB; AAZ08134.
 XX New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.

XX Claim 22; Page 67; 71pp; English.

XX The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Gln1Ser. Carboxy terminal end of
 CC recombinant RaCOR1 has a covalently bound ligand binding moiety, which
 CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
 CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
 CC Recombinant ribonucleases can be expressed in bacteria without an N-
 CC terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases

SQ Sequence 110 AA;

Query Match 99.2%; Score 597; DB 2; Length 110;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:25:55 ; Search time 46.9224 Seconds
(without alignments)
662.376 Million cell updates/sec

Title: US-09-961-400-15

Perfect score: 602

Sequence: 1 QNWFQKXHIINPIICNT.....ICVKCNQYPVHFAGIGRCF 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	602	100.0	110	2	AA28872 Rana cate
2	602	100.0	111	2	AA28873 Recombina
3	597	99.2	110	2	AA28877 Recombina
4	597	99.2	111	2	AA28878 Recombina
5	596	99.0	110	2	AA28874 Recombina
6	596	99.0	111	2	AA28876 Recombina
7	588.5	97.8	111	2	AA28877 Recombina
8	284.5	47.3	104	2	AA28878 Recombina
9	281.5	46.8	104	2	AA28879 Recombina
10	281.5	46.8	105	2	AA28877 Recombina
11	281.5	46.8	105	2	AA28879 Recombina
12	278.5	46.3	104	2	AA28866 Recombina
13	278.5	46.3	105	2	AA28869 Recombina
14	277.5	46.1	104	2	AA28870 Recombina
15	277.5	46.1	104	2	AA28871 Recombina
16	277.5	46.1	104	2	AA28872 Recombina
17	277.5	46.1	105	2	AA28873 Recombina
18	277.5	46.1	105	2	AA28874 Recombina
19	276.5	45.9	104	2	AA28875 Recombina
20	276.5	45.9	105	2	AA28876 Recombina
21	274.5	45.6	104	2	AA28877 Recombina
22	274.5	45.6	104	2	AA28878 Recombina
23	274.5	45.6	104	2	AA28879 Recombina
24	274.5	45.6	104	2	AA28880 Recombina
25	274.5	45.6	104	2	AA28881 Recombina

26	274.5	45.6	104	2	AAW88233 Rana pipi
27	274.5	45.6	104	2	AA33322 Prog onco
28	274.5	45.6	105	2	AAW35123 R. pipien
29	274.5	45.6	355	2	AAW35125 R. pipien
30	274.5	45.6	358	2	AAW35130 R. pipien
31	272.5	45.3	104	4	AA31667 Amino aci
32	272.5	45.3	104	5	AB31617 Northern
33	272.5	45.3	106	2	AAW35122 R. pipien
34	272.5	45.3	107	2	AAW35117 R. pipien
35	272.5	45.3	112	2	AAW35118 R. pipien
36	272.5	45.3	251	2	AAW35134 R. pipien
37	272.5	45.3	254	2	AAW35135 R. pipien
38	272.5	45.3	355	2	AAW35133 R. pipien
39	272.5	45.3	355	2	AAW35129 R. pipien
40	272.5	45.3	366	2	AAW35132 R. pipien
41	271.5	45.1	104	2	AAW30302 Recombina
42	267.5	44.4	104	2	AAW18224 Antitumou
43	267.5	44.4	105	2	AAW35115 R. pipien
44	267.5	44.4	105	2	AAW35116 R. pipien
45	263.5	43.8	358	2	AAW35127 R. pipien

ALIGNMENTS

RESULT 1

AA28872
ID AA28872 standard; protein; 110 AA.

XX AC AA28872;

XX DT 25-JAN-2000 (first entry)

XX DE Rana catesbeiana oocyte ribonuclease (RACOR1) amino acid sequence.

XX KW Rana catesbeiana oocyte ribonuclease; RACOR1; covalently bound; CD22;
XX KW LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;
XX KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog;
XX KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
XX KW RNase.

XX OS Rana catesbeiana.

XX QS Synthetic.

XX PN WC9950398-A2.

XX XX WO9950398-A2.

XX PD 07-OCT-1999.

XX PF 26-MAR-1999; 99WO-US006641.

XX PR 27-MAR-1998; 98US-0079751P.

XX XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PA Rybak SM, Newton DL;

XX PI WPI; 1999-610847/52.

XX DR N-FSDB; AA208130.

XX XX New recombinant ribonucleases, used for killing target cells, e.g. for

XX XX treating cancers, viral infections or autoimmune diseases.

XX XX Claim 22; Page 62; 71pp; English.

XX CC The present sequence is a Rana catesbeiana oocyte ribonuclease (RACOR1)

XX CC protein encoded by a cDNA modified for expression in E. coli. Carboxy

XX CC terminal end of RACOR1 has a covalently bound ligand binding moiety,

XX CC which can be a LL2 antibody directed against CD22 on cancerous B cells or

XX CC human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma

XX CC cells. Recombinant ribonucleases can be expressed in bacteria without an

XX CC N-terminal methionine due to the presence of a signal peptide that is

XX CC cleaved by bacteria. The soluble expression of ribonuclease allows the

XX CC proteins to be fused in-frame with ligand binding moieties to form

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; U22516; AAA91366.1; -.
DR EMBL; BC055355; AAH55355.1; -.
DR PIR; A35932; A35932.
DR HSSP; P03950; 1A4Y.
DR MGD; MGI:88022; Arg.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PRO0794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase Pc; 1.
DR PROSITE; PS0127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
SQ SEQUENCE 145 AA; 16228 MW; 06944260BB764938 CRC64;
ANGIOGENIN.
PYRROLIDONE CARBOXYLIC ACID (BY
SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

Query Match 20.5%; Score 119.5; DB 1; Length 145;
Best Local Similarity 30.8%; Pred. No. 6.5e-06;
Matches 33; Conservative 12; Mismatches 45; Indels 17; Gaps 5;
QY 10 KHLTWTROVD-----CNIIMSTNLF--HCKDKNTFIYSRPEVKAIC--KGIASKN 57
Db 32 KFLTQHDAKPKGRDDRYCERWMKRRSLTSPCKDVNTFIHGKSNKAIKCGANGSPYREN 91
QY 58 V-LTISEFYISDCNVT-----RPFCKYKLLKSTNTFCVTCENQAPVHF 99
Db 92 LEMSKSPFQVTTCKHTGGSPPPCQYRASAGFRHVVIAENGULPVHF 138

Search completed: May 7, 2004, 21:53:05
Job time : 5.30402 secs


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FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .).
FT VARIANT 64 64 L -> P.
SQ SEQUENCE 128 AA; 14406 MW; 42F4101A1A33E93B CRC64;

Query Match
Best Local Similarity 20.6%; Score 120; DB 1; Length 128;
Matches 35; Conservative 21; Mismatches 37; Indels 30; Gaps 7;

QY 2 SDMLTFQKKHL-----TNRDVCNNIM-----STNLFHCKDKNTFIYSRPEPVKAICKGI 52
DB 3 SSAMKFORQHMDEGSPSPSSNY-CNVMIRNMTQGRCKPVNTFVHESLADVOAVC--- 58
QY 53 IASKNVL-----TTSEFVLSDCNVTSRP-----CKYKLLKSTNTFCVTCENQ--AP 96
DB 59 -FQKNVLCKNGQTCYQSYSRMRITDCRVTSSSSEFPCNSRMSQAQKSIIVACGEGPYVP 117
QY 97 VHF 99
DB 118 VHF 120

RESULT 14
RNP PROGU STANDARD; PRT; 128 AA.
AC P04059;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Proechimys guairae (Casiragua).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Echimyidae; Proechimys.
ON NCBI_TaxID=10163;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=83000399; PubMed=7115727;
RA Beintema J.J., Krol G., Martena B.;
RT "The primary structures of pancreatic ribonucleases from African
RL porcupine and casiragua, two hystricomorph rodent species.";
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2', 3'-cyclic phosphate intermediates.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Pancreas.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR; A00821; NRKS.
DR HSP; P00656; 1SRN.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR PRINTS; P00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase P; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 128 AA; 14244 MW; 2DB5803A9D3C936 CRC64;

Query Match
Best Local Similarity 20.6%; Score 120; DB 1; Length 128;
Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

QY 7 FQKKHL-----TNRDVCNNIM-STNLF-HCKKNTFIYSRPEPVKAICKGIITASKNV 58

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Db 8 FQKHIDSSGSPSTNPNYCNAMKSRNMTQGRCKPVNTFVHEPLADVOAVC-----FQKNV 63
QY 59 -----LTTSEFVLSDCNVTSR-----PCYKLLKKSINTFCVTCENQ--APVHF 99
Db 64 PCXNGQSNVCYESTSNMHTDCLUTSNKSPDCLYRTSQEKSIIIVACGPNYPVHF 120

RESULT 15
ANGI MOUSE
ID ANGI_MOUSE STANDARD; PRT; 145 AA.
AC P21570;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91025023; PubMed=2222458;
RA Bond M.D., Vallee B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N, TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fainley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP PARTIAL SEQUENCE.
RP TISSUE=Serum;
RX MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
RT angiogenins: discernment of functionally important residues and
RT regions.";
RL Biochim. Biophys. Acta 1162:177-186(1993).
CC -!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
CC angiogenin is endocytosed and translocated to the nucleus, thereby
CC promoting the endothelial invasiveness necessary for blood vessel
CC formation. Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

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DR InterPro; IPR001427; RNaseA.
DR Pfam; PF000074; rnaaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 76 N-LINKED (GLCNAC...) (30%).
SQ SEQUENCE 124 AA; 14125 MW; F57475459F697E20 CRC64;

Query Match 21.5%; Score 125; DB 1; Length 124;
Best Local Similarity 28.6%; Pred. No. 1.4e-06;
Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;

QY 5 LTFQKKHLTNTRDVID-----CNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASK 56
DB 6 MKFQHQHDSGNSPNNPNYCNQMMRRKKTQGRCKPVNTFVHSELDVKAVC-----SQK 61
QY 57 NVL-----TTFEYLSDCNVTSRP-----CKYKLKXSTNTPCVTCENQ--APVHF 99
DB 62 NVLCKNGRTNCYESNSTMHTDCRQTGSGSKYPNCAYKTSQKEKHIIIVACGNPVYPVHF 120

RESULT 12
ANGI_MACMU
ID ANGI_MACMU STANDARD; PRT; 146 AA.
AC Q8WN63;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin precursor (BC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG OR RNASE5.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OC NCBI_TaxID=9544;
RP [1]
SEQUENCE FROM N.A.
RX MEDLINE=21918422; PubMed=11919285;
RA Zhang J., Rosenberg H.F.;
RT "Diversifying selection of the tumor-growth promoter angiogenin in
RT primate evolution.";
RL Mol. Biol. Evol. 19:438-445(2002).
CC -!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
CC to actin on the surface of endothelial cells; once bound,
CC angiogenin is endocytosed and translocated to the nucleus, thereby
CC promoting the endothelial invasiveness necessary for blood vessel
CC formation. Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF416667; AAL61649.1; -.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF000074; rnaaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.

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DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 24 BY SIMILARITY.
FT CHAIN 25 146 ANGIOGENIN.
FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT ACT_SITE 138 138 BY SIMILARITY.
FT DISULFID 50 105 BY SIMILARITY.
FT DISULFID 63 116 BY SIMILARITY.
FT DISULFID 81 131 BY SIMILARITY.
SQ SEQUENCE 146 AA; 16301 MW; E39A89215DB2A2A4 CRC64;

Query Match 20.9%; Score 121.5; DB 1; Length 146;
Best Local Similarity 28.7%; Pred. No. 4e-06;
Matches 29; Conservative 17; Mismatches 32; Indels 23; Gaps 4;

QY 6 TFOKKHLTNTRDVIDCNIMSTNLFHCKDKNTFIYSRPEPVKAIC---KGIIASKNV-LTT 61
DB 53 TMRERHLTSP-----CKDINIFVHGRRHHTAICDENGSPYGGNLRIST 97
QY 62 SEFYLSDCNVTS-----RPCKYKLKXSTNTPCVTCENQAPVH 98
DB 98 SPFOVTTCKURGGSPRPCCQYRATRGSRNIVVGCENGLPVH 138

RESULT 13
RNBP_CAVPO
ID RNBP_CAVPO STANDARD; PRT; 128 AA.
AC P00679;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic B (EC 3.1.27.5) (RNase IB).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OC NCBI_TaxID=10141;
RP [1]
SEQUENCE
TC TISSUE=Pancreas;
RX MEDLINE=77185023; PubMed=862624;
RA van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gaastra W.,
RA Beintema J.J.;
RT "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary
RT structure and glycosylation.";
RL Eur. J. Biochem. 75:91-100(1977).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3',-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Pancreas.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR; A00826; NRGPB.
DR HSSP; P00656; 1SRN.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF000074; rnaaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.

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RT "Solution structure of bovine angiogenin by 1H nuclear magnetic
RL resonance spectroscopy."
RL Biochemistry 35:8870-8880(1996).
CC -!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
CC to actin on the surface of endothelial cells; once bound,
CC angiogenin is endocytosed and translocated to the nucleus, thereby
CC promoting the endothelial invasiveness necessary for blood vessel
CC maturation. Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular rRNAs. Binds tightly to placental
CC ribonuclease inhibitor and has very low ribonuclease activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Serum and milk.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF135124; AAG47631.1; -.
CC PDB: 1AGI; 03-APR-96.
CC PDB: 1GIO; 07-DEC-96.
CC InterPro: IPR001427; RNaseA.
CC Pfam: PF00074; RNaseA; 1.
CC PRINTS: PR00794; RIBONUCLEASE.
CC ProDom: PD000535; RNaseA; 1.
CC SMART: SM00092; RNaseA; 1.
CC PROSITE: PS00127; RNASE PANCREATIC; 1.
CC Hydrolase; Nuclease; Endonuclease; Angiogenesis;
CC Protein synthesis inhibitor; Signal; 3D-structure.
CC
CC FT SIGNAL 1 23 ANGIOGENIN-1.
CC CHAIN 24 148
CC FT ACT SITE 37 37
CC FT ACT SITE 64 64
CC FT ACT SITE 138 138
CC FT DISULFID 50 105
CC FT DISULFID 63 116
CC FT DISULFID 81 131
CC SEQUENCE 148 AA; 16969 MW; B7999124CBB523DD CRC64;

Query Match 22.0%; Score 128; DB 1; Length 148;
Best Local Similarity 34.0%; Pred. No. 8.3e-07;
Matches 33; Conservative 14; Mismatches 32; Indels 19; Gaps 5;

QY 17 DVDQNNIMSTNLF--HCKDKNTFIYSRPEPVKAICKGLIASKNV 66
DB 47 DEYCFNMKNRLTRPCKDRNTFIHGNKNIDKAICE---DRNGQFYRGDLRIKSEFQI 102
QY 67 SDC---NVTSR--PKYKLLKKNSTNTFCVTCENQAPVHF 99
DB 103 TICKHKGSSRPPCRYGATEDSRVIVGCGNGLPVHF 139

RESULT 10
RNP MYOCO
ID - RNP MYOCO STANDARD; PRT; 128 AA.
AC P00676;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Myocastor coypu (Coypu) (Nutria).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Myocastoridae;
OC Myocastor.
OX NCBI_TaxID=10157;
RN [1]
RP SEQUENCE.

MEDLINE=76277855; PubMed=962870;
RA Emmens M., Welling G.W., Beintema J.J.;
RT "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
RT ribonuclease."
RL Biochem. J. 157:317-323(1976).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Pancreas.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC PIR; A00819; NRWHK.
CC HSSP; P00656; ISRN.

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TISSUE=Pancreas;
MEDLINE=77065676; PubMed=999896;
RA van den Berg A., van den Hende-Timmer L., Beintema J.J.;
RT "Isolation, properties and primary structure of coypu and chinchilla
RT pancreatic ribonuclease."
RL Biochim. Biophys. Acta 453:400-409(1976).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Pancreas.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC PIR; A00822; NRCU.
CC HSSP; P00656; ISRN.
CC InterPro: IPR001427; RNaseA.
CC Pfam: PF00074; RNaseA; 1.
CC PRINTS: PR00794; RIBONUCLEASE.
CC ProDom: PD000535; RNaseA; 1.
CC SMART: SM00092; RNaseA; 1.
CC PROSITE: PS00127; RNASE PANCREATIC; 1.
CC Hydrolase; Nuclease; Endonuclease; Glycoprotein.
CC DISULFID 26 84
CC DISULFID 40 95
CC DISULFID 58 110
CC DISULFID 65 72
CC ACT SITE 12 12
CC ACT SITE 41 41
CC ACT SITE 119 119
CC CASBOHYD 34 34
CC SEQUENCE 128 AA; 14267 MW; 4EB924E52B445832 CRC64;

Query Match 21.6%; Score 126; DB 1; Length 128;
Best Local Similarity 29.9%; Pred. No. 1.1e-06;
Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

QY 7 FQKQHL-----TNRDVEDCNIM--STNLF--HCKDKNTFIYSRPEPVKAICKGLIASKNV 58
DB 8 FERQHMDSRGSPSTPNYCNEMMKSRNNTQCRKPVNTFVHEPLADVOAVC----FQKNV 63
QY 59 L-----TTSEFVLSDCNVTSRP-----CKYKLLKKNSTNTFCVTCENQ--APVHF 99
DB 64 LCKNGQTCYQSNMNHITDCRVTSNSDYPNCSYRTSQEKSIVVACBGNFVPVHF 120

RESULT 11
RNP BALAC
ID - RNP BALAC STANDARD; PRT; 124 AA.
AC P00673;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaenopteridae; Balaenoptera.
OX NCBI_TaxID=9767;
RN [1]
RP SEQUENCE.

MEDLINE=76277855; PubMed=962870;
RA Emmens M., Welling G.W., Beintema J.J.;
RT "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
RT ribonuclease."
RL Biochem. J. 157:317-323(1976).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Pancreas.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC PIR; A00819; NRWHK.
CC HSSP; P00656; ISRN.

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FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT ACT_SITE 137 137 BY SIMILARITY.
FT DISULFID 50 104 BY SIMILARITY.
FT DISULFID 63 115 BY SIMILARITY.
FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429C4D CRC64;

Query Match 22.4%; Score 130.5; DB 1; Length 145;
Best Local Similarity 38.2%; Pred. No. 4.4e-07;
Matches 29; Conservative 11; Mismatches 29; Indels 7; Gaps 3;

QY 31 CKDKNFTFYSPPEPVKAIC--KGIASKNV-LTTSEFYLSDCNVTSR-----PCKYKLKKS 83
DB 63 CKDNTFTHTKNNKAIKCGKSPYGNLRISKSRFQVTTCTHKGRSPRPQRYASKG 122
QY 84 TNTFCVTENQAPVHF 99
DB 123 FRYIIIGENGWVPHF 138

RESULT 8
ANGI CERAE
ID ANGI CERAE STANDARD; PRT; 146 AA.
AC O8WN66;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG OR RNASES.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21918422; PubMed=11919285;
RA Zhang J., Rosenberg H.P.;
RT "Diversifying selection of the tumor-growth promoter angiogenin in
RT primate evolution.";
RL Mol. Biol. Evol. 19:439-445(2002).
CC -1- FUNCTION: May function as a tRNA-specific ribonuclease that binds
CC to actin on the surface of endothelial cells; once bound,
CC angiogenin is endocytosed and translocated to the nucleus, thereby
CC promoting the endothelial invasiveness necessary for blood vessel
CC formation. Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC -----
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CC -----
DR EMBL; AF441664; AAL61646.1;
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00127; RNASE_PANCREATIC; 1.
DR PROSITE; PS00092; RNASE_Pc; 1.
KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 24 BY SIMILARITY.
FT CHAIN 25 146 ANGIOGENIN.
FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).

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FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT ACT_SITE 138 138 BY SIMILARITY.
FT DISULFID 50 105 BY SIMILARITY.
FT DISULFID 63 116 BY SIMILARITY.
FT DISULFID 81 131 BY SIMILARITY.
SQ SEQUENCE 146 AA; 16444 MW; 27860112E85B8DF9 CRC64;

Query Match 22.4%; Score 130.5; DB 1; Length 146;
Best Local Similarity 30.7%; Pred. No. 4.4e-07;
Matches 31; Conservative 17; Mismatches 30; Indels 23; Gaps 4;

QY 6 TFOKKHLNTRDVCNIMSTNLPHCKDKNFIYSRPFVKAIC---KGIASKNV-LTT 61
DB 53 TMRKRLHLSF-----CKDINTFIHGRHHIKAICDGENGPNYPGENLRISK 97
QY 62 SEFYLSDCNVTST----RPCKYKLKKSNTFCVTENQAPVH 98
DB 98 SPFQVTTCLRGSGSPRPFCQYRATRGSRNIVVGCENGLPVH 138

RESULT 9
ANGI BOVIN
ID ANGI BOVIN STANDARD; PRT; 148 AA.
AC P10152; O9GKP9;
DT 01-MAR-1989 (Rel. 10, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Angiogenin-1 precursor (EC 3.1.27.-).
GN ANG1 OR ANG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Chang S.-I.;
RT "Cloning, sequencing, and expression of bovine angiogenin.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC [2]
CC SEQUENCE OF 24-148.
CC TISSUE=Milk;
CC MEDLINE=89065101; PubMed=3197838;
CC Maes P., Damart D., Rommens C., Montreuil J., Spik G., Tartar A.;
CC "The complete amino acid sequence of bovine milk angiogenin.";
CC FEBS Lett. 241:41-45(1988).
CC [3]
CC SEQUENCE OF 24-148.
CC TISSUE=Plasma;
CC MEDLINE=89375344; PubMed=2775757;
CC Bond M.D., Strydom D.J.;
CC "Amino acid sequence of bovine angiogenin.";
CC Biochemistry 28:6110-6113(1989).
CC [4]
CC CHARACTERIZATION, AND SEQUENCE OF 25-55.
CC TISSUE=Plasma;
CC MEDLINE=89118214; PubMed=3064806;
CC Bond M.D., Vallee B.L.;
CC "Isolation of bovine angiogenin using a placental ribonuclease
CC inhibitor binding assay";
CC Biochemistry 27:6282-6287(1988).
CC [5]
CC X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
CC MEDLINE=95224057; PubMed=7708754;
CC Acharya K.R., Shapiro R., Riordan J.F., Vallee B.L.;
CC "Crystal structure of bovine angiogenin at 1.5-A resolution.";
CC Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).
CC [6]
CC STRUCTURE BY NMR.
CC MEDLINE=96280645; PubMed=8688423;
CC Lequin O., Albarret C., Bontems F., Spik G., Lallemand J.-Y.;

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QY 3 DWTTFQKKHLNTRDVCNNIMSTNLF-----HCKDKNTFYSRPEPVKAICKGIASKNV 58
Db 24 NWAATFOQKHILNTRDVCNNIMSTNLF-----HCKDKNTFYSRPEPVKAICKGIASKNV 82
QY 59 LTTSEFYLSDC---NVTSRPKYKLLKSTNTFCVTCEQAPVHFVGVGHC 105
Db 83 LSTTRFQNTCTRTSITPRPCPYSSRTETNIVKRCENQYPVHFAGIGRC 132

RESULT 3
ID LECs_RANJA STANDARD; PRT; 111 AA.
AC P18839;
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sialic acid-binding lectin (EC 3.1.27.-).
OS Rana japonica (Japanese redbell frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Egg;
RX MEDLINE=91035319; PubMed=2229005;
RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
RA Takayanagi Y., Titani K.;
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT eggs.";
RL J. Biochem. 108:139-143(1990).
CC -!- FUNCTION: The S-lectins in frog eggs may be involved in the
CC fertilization and development of the frog embryo. This lectin
CC preferentially agglutinate a large variety of tumor cells, but it
CC does not agglutinate non-transformed cells and erythrocytes.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR HSP; P11916; IBC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease; Sialic acid; Lectin;
KW Pyridolone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 35 35 BY SIMILARITY.
FT ACT_SITE 104 104 BY SIMILARITY.
FT DISULFID 19 72 BY SIMILARITY.
FT DISULFID 34 82 BY SIMILARITY.
FT DISULFID 52 97 BY SIMILARITY.
FT DISULFID 94 111 PROBABLE.
SQ SEQUENCE 111 AA; 12326 MW; FDEBDF3834ED679 CRC64;

Query Match 48.2%; Score 280.5; DB 1; Length 111;
Best Local Similarity 44.5%; Pred. No. 3.1e-23;
Matches 49; Conservative 19; Mismatches 35; Indels 7; Gaps 2;

QY 3 DWTTFQKKHLNTRDVCNNIMSTNLF-----HCKDKNTFYSRPEPVKAICKGIASKNV 58
Db 2 NWAATFOQKHILNTRDVCNNIMSTNLF-----HCKDKNTFYSRPEPVKAICKGIASKNV 58
QY 59 LTTSEFYLSDC---NVTSRPKYKLLKSTNTFCVTCEQAPVHFVGVGHC 105
Db 83 LSTTRFQNTCTRTSITPRPCPYSSRTETNIVKRCENQYPVHFAGIGRC 132

RESULT 4
ID RNPL_RANCA STANDARD; PRT; 111 AA.
AC P14626;
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sialic acid-binding lectin (EC 3.1.27.-).
OS Rana japonica (Japanese redbell frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Liver;
RX MEDLINE=90130374; PubMed=2613682;
RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
RA Okazaki T., Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
RT liver.";
RL J. Biochem. 106:729-735(1989).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR HSP; P11916; IBC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease; Pyridolone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 35 35 BY SIMILARITY.
FT ACT_SITE 104 104 BY SIMILARITY.
FT DISULFID 19 72 BY SIMILARITY.
FT DISULFID 34 82 BY SIMILARITY.
FT DISULFID 52 97 BY SIMILARITY.
FT DISULFID 94 111 PROBABLE.
SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 45.4%; Score 264.5; DB 1; Length 111;
Best Local Similarity 42.7%; Pred. No. 1.6e-21;
Matches 47; Conservative 19; Mismatches 37; Indels 7; Gaps 2;

QY 3 DWTTFQKKHLNTRDVCNNIMSTNLF-----HCKDKNTFYSRPEPVKAICKGIASKNV 58
Db 2 NWAATFOQKHILNTRDVCNNIMSTNLF-----HCKDKNTFYSRPEPVKAICKGIASKNV 58
QY 59 LTTSEFYLSDC---NVTSRPKYKLLKSTNTFCVTCEQAPVHFVGVGHC 105
Db 62 LSTTRFQNTCTRTSITPRPCPYSSRTETNIVKRCENQYPVHFAGIGRC 111

RESULT 5
ID RNP_IGUIG STANDARD; PRT; 119 AA.
AC P80287;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
OS Iguana iguana (Common iguana).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosaurs; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX NCBI_TaxID=8517;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=94139745; PubMed=8307028;
RA Zhao W., Beintema J.J., Hofsteenge J.;
RT "The amino acid sequence of iguana (Iguana iguana) pancreatic
RT ribonuclease.";
RL Eur. J. Biochem. 219:641-646(1994).

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FT DISULFID 48 90
FT DISULFID 87 104
FT HELIX 3 10
FT STRAND 11 12
FT HELIX 19 22
FT TURN 23 24
FT TURN 26 30
FT STRAND 33 38
FT HELIX 41 45
FT HELIX 46 48
FT TURN 49 50
FT STRAND 55 58
FT STRAND 63 70
FT TURN 74 75
FT STRAND 77 84
FT STRAND 86 91
FT TURN 92 93
FT STRAND 94 101
SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match 94.7%; Score 551; DB 1; Length 104;
Best Local Similarity 96.1%; Pred. No. 3.9e-52;
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 DWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAIKGIASKNVLTTS 62
DB 2 DWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAIKGIASKNVLTTS 61
QY 63 EFLYSDCNVTRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
DB 62 EFLYSDCNVTRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 2
ID RNPO RANCA STANDARD; PRT; 133 AA.
AC P11916; Q9PWR7;
DT 01-OCT-1989 (Rel. 12, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-
DE binding lectin) (SBL-C).
GN RCR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98165825; PubMed=9497370;
RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
RT Tissue distribution, cloning, purification, cytotoxicity, and active
RT residues for RNase activity."
RL J. Biol. Chem. 273:6395-6401(1998).
RN [2]
RP SEQUENCE OF 23-133.
RC TISSUE=Egg;
RX MEDLINE=87299649; PubMed=3304421;
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
RA Takayanagi G., Hakomori S.;
RT "Amino acid sequence of sialic acid binding lectin from frog (Rana
RT catesbeiana) eggs."
RL Biochemistry 26:2189-2194(1987).
RN [3]
RP CHARACTERIZATION, AND SEQUENCE OF 81-101.
RX MEDLINE=92220613; PubMed=1373237;
RA Liao Y.-D.;
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana
RT catesbeiana (bullfrog) oocytes."
RL Nucleic Acids Res. 20:1371-1377(1992).
RN [4]
```

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RP CHARACTERIZATION.
RC TISSUE=Egg;
RX MEDLINE=93192604; PubMed=8448385;
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
RA Takayanagi Y., Hakomori S., Titani K.;
RT "Ribonuclease activity of sialic acid-binding lectin from Rana
RT catesbeiana eggs."
RL Glycobiology 3:37-45(1993).
RN [5]
RP STRUCTURE BY NMR OF 23-133.
RX MEDLINE=98437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
RT "The solution structure of a cytotoxic ribonuclease from the oocytes
RT of Rana catesbeiana (bullfrog)."
RL J. Mol. Biol. 283:231-244(1998).
CC -!- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine
CC residues with a 3' flanking guanine. Hydrolyzes poly(U) and poly(C)
CC as substrates, and prefers the former. The S-lectins in frog eggs
CC may be involved in the fertilization and development of the frog
CC embryo. This lectin agglutinates various animal cells, including
CC normal lymphocytes, erythrocytes, and fibroblasts of animal and
CC human origin. It is cytotoxic against several tumor cells.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF039104; AAD10702.1; -.
DR FIR; A27121; A27121.
DR PDB; 1BC4; 28-OCT-98.
DR PDB; 1M07; 21-JAN-03.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
KW Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 22
FT CHAIN 23 133 RIBONUCLEASE, OOCYTES.
FT MOD RES 23 23 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 32 32
FT ACT_SITE 57 57
FT ACT_SITE 125 125
FT ACT_SITE 41 93
FT DISULFID 56 103
FT DISULFID 74 118
FT DISULFID 115 132
FT HELIX 25 32
FT HELIX 41 45
FT TURN 48 49
FT STRAND 59 63
FT HELIX 67 73
FT TURN 74 74
FT STRAND 79 84
FT STRAND 90 95
FT STRAND 105 110
FT STRAND 114 119
FT TURN 120 121
FT TURN 122 129
SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;

Query Match 49.3%; Score 287; DB 1; Length 133;
Best Local Similarity 49.1%; Pred. No. 7.8e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:30:40 ; Search time 5.30402 Seconds
(without alignments)
1030.796 Million cell updates/sec

Title: US-09-961-400-13

Perfect score: 582

Sequence: 1 MSDWLTFQKHLNTRDVDC.....TFCVTCENQAPVHFVGWGHG 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551	94.7	104	1	RN30_RANPI
2	287	49.3	133	1	RNPO_RANCA
3	280.5	48.2	111	1	LECS_RANJA
4	264.5	45.4	111	1	RNPL_RANCA
5	144	24.7	119	1	RNP_IGUIG
6	132	22.7	124	1	RNP_GALMU
7	130.5	22.4	145	1	ANGR_MOUSE
8	130.5	22.4	146	1	ANGI_CERAE
9	128	22.0	148	1	ANGI_BOVIN
10	126	21.6	128	1	RNP_MYOCC
11	125	21.5	124	1	RNP_BALAC
12	121.5	20.9	146	1	ANGI_MACMU
13	120	20.6	128	1	RNPB_CAVPO
14	120	20.6	128	1	RNP_PROGU
15	119.5	20.5	145	1	ANGI_MOUSE
16	118.5	20.4	146	1	ANGI_PAPHA
17	118	20.3	124	1	RNP_CHIBR
18	117	20.1	128	1	RNP_HYDHY
19	116	19.9	125	1	ANGI_RABIT
20	115	19.8	146	1	ANGI_MIOTA
21	114	19.6	124	1	RNP_HIPAM
22	113.5	19.5	147	1	RNS4_PANTR
23	113	19.4	147	1	ANGI_HUMAN
24	113	19.4	147	1	ANGI_PANTR
25	113	19.4	156	1	ECF3_MOUSE
26	112	19.2	124	1	RNP_FIG
27	112	19.2	128	1	RNP_HYSCR
28	112	19.2	150	1	RNP_BOVIN
29	112	19.2	156	1	RNP_MYOGL
30	111.5	19.2	147	1	RNS4_HUMAN
31	111	19.1	128	1	RNP_HORSE
32	111	19.1	146	1	ANGI_SAISC
33	111	19.1	167	1	RNBR_BOVIN

34 110.5 19.0 123 1 ANGI_PIG
35 110.5 19.0 155 1 ECF1_MOUSE
36 110 18.9 124 1 RNPA_CAVPO
37 110 18.9 141 1 RNBR_GIRCA
38 110 18.9 146 1 ANGI_SAGOE
39 110 18.9 151 1 RNBR_AXIPR
40 110 18.9 156 1 ECF2_MOUSE
41 109 18.7 123 1 ANG2_BOVIN
42 109 18.7 124 1 RNP_AEPME
43 109 18.7 124 1 RNP_ANTAM
44 109 18.7 124 1 RNP_SHEEP
45 108.5 18.6 150 1 RNS6_SAISC

ALIGNMENTS

RESULT 1
RN30_RANPI
AC P22069;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE P-30 protein (EC 3.1.27.-) (Onconase)
OS Rana pipiens (Northern leopard frog)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=91093131; PubMed=985896;
RA Ardelit W., Mikulski S.M., Shogen K.;
RT "Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";
RL J. Biol. Chem. 266:245-251(1991).
RN [2]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=93066156; PubMed=1438177;
RA Mosimann S.C., Johns K.L., Ardelit W., Mikulski S.M., Shogen K., James M.N.G.;
RT "Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens oocytes and early embryos.";
RL Proteins 14:392-400(1992).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX MEDLINE=94166079; PubMed=8120892;
RA Mosimann S.C., Ardelit W., James M.N.G.;
RT "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";
RL J. Mol. Biol. 236:1141-1153(1994).
CC -!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity against several tumor cell lines in vitro, as well as antitumor in vivo. It exhibits a ribonuclease-like activity against high molecular weight ribosomal RNA.
CC -!- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PDB; IONC; 3I-JAN-94.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; 3D-structure;
KW Pyrolidone carboxylic acid. PYROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT ACT_SITE 10 10
FT ACT_SITE 31 31
FT ACT_SITE 97 97
FT DISULFID 19 68
FT DISULFID 30 75

P31346 sus scrofa
P97426 mus musculus
P00678 cavia porce
Q29542 giraffa cam
Q8wn62 saguinus oe
P87350 axis porcin
P97425 mus musculus
P80929 bos taurus
P07847 aepyceros m
P00668 antilocapra
P00661 ovnis aries
O46529 salmimi sci

Search completed: May 7, 2004, 21:54:54
Job time : 9.5276 secs

Query Match 20.6%; Score 120; DB 1; Length 128;
Best Local Similarity 29.9%; Pred. No. 5.3e-05;
Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;
QY 7 FQKHL-----TNRDVCNNIM--STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV 58
DB 8 FQCHIDSSGSPSTPNFYCNAMKRNMTQERCKPNTFVHEPLADVQAVC-----FQKNV 63
QY 59 -----LTTSEFYLSDCNVTSR-----PCKYKLKSKTNTFCVTCENQ--APVHF 99
DB 64 PCKNGQSNVCYSTSNHHTDCLTNSKPPDCLYRTSOEBSIIVACEGNPVVPVHF 120
RESULT 11
NRGPB
pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
N:Alternate names: RNase IB
C:Species: Cavia porcellus (guinea pig)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A00826
R:van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J.
Biochem. J. Biochem. 75, 91-100, 1977
A:Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure
A:Reference number: A91247; MUID:77185023; PMID:862624
C:Accession: A00826
A:Molecule type: protein
A:Residues: 1-128 <VAN>
A:Note: 64-Pro was also found
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12.41.119/Active site: His, Lys, His #status predicted
F:21.34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:26-84, 40-95, 58-110, 65-72/Disulfide bonds: #status predicted
Query Match 20.6%; Score 120; DB 1; Length 128;
Best Local Similarity 28.5%; Pred. No. 5.3e-05;
Matches 35; Conservative 21; Mismatches 37; Indels 30; Gaps 7;
QY 2 SDWLTFQKHL-----TNRDVCNNIM--STNLFHCKDKNTFIYSRPEPVKAICKGI 52
DB 3 SSAMKFORQHMDSGSPSSNY--CNVMIRNMTQGRCKPNVTFHESLADVQAVC--- 58
QY 53 IASKNV-----TTSEFYLSDCNVTSR-----CKYKLKSKTNTFCVTCENQ--AP 96
DB 59 -FQKNVCKNGQTCYQYSRMTDCLRTSSSKFPNCYSRMSQAQKSIIVACEGDPVP 117
QY 97 VHF 99
DB 118 VHF 120
RESULT 12
A35932
angiogenin precursor - mouse
N:Alternate names: angiogenesis factor
N:Contains: ribonuclease (EC 3.1.27.-)
C:Species: Mus musculus (house mouse)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C:Accession: A35932
R:Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A:Title: Isolation and sequencing of mouse angiogenin DNA.
A:Reference number: A35932; MUID:91025023; PMID:222458
C:Accession: A35932
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-145 <BON>
A:Cross-references: GB:U22516; NID:G726325; PIDN:AAA91366.1; PID:G726326
C:Genetics:
A:Introns: #status absent
C:Function:
A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C:Superfamily: pancreatic ribonuclease

C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-145/Product: angiogenin #status predicted <MAT>
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:37.64.137/Active site: His, Lys, His #status predicted
F:50-104, 63-115, 81-130/Disulfide bonds: #status predicted
Query Match 20.5%; Score 119.5; DB 1; Length 145;
Best Local Similarity 30.8%; Pred. No. 6.8e-05;
Matches 33; Conservative 12; Mismatches 45; Indels 17; Gaps 5;
QY 10 KHLNTRDVC-----CNNIMSTNLF--HCKDKNTFIYSRPEPVKAIC--KGIASKN 57
DB 32 KFLTQHDAKPKGRDDRYCERMKRSRLTSFCKDVTFIHGKSNKAIKCGANGSPYREN 91
QY 58 V-LTTSEFYLSDCNVT-----RPCKYKLKSKTNTFCVTCENQAPVHF 99
DB 92 LRMSKSPFQVTTCKHTGSGPRPCQYRASAGFRHVVIACENGLPVHF 138
RESULT 13
NRGPB
pancreatic ribonuclease (EC 3.1.27.5) - Chinchilla brevicaudata (tentative sequence)
N:Alternate names: RNase A
C:Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata
C:Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C:Accession: A00820
R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A:Reference number: A90612; MUID:77065676; PMID:999896
C:Accession: A00820
A:Molecule type: protein
A:Residues: 1-124 <VAN>
A:Note: a second component of chinchilla ribonuclease has 32-Asp
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12.41.119/Active site: His, Lys, His #status predicted
F:26-84, 40-95, 58-110, 65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 20.3%; Score 118; DB 1; Length 124;
Best Local Similarity 27.0%; Pred. No. 8.2e-05;
Matches 33; Conservative 19; Mismatches 42; Indels 28; Gaps 6;
QY 2 SDWLTFQKHL-----TNRDVCNNIM--STNLFHCKDKNTFIYSRPEPVKAICKGII 53
DB 3 SSAMKFORQHMDSGSPSTNANYCNEMMKGRNMTQGYCKPNTFVHEPLADVQAVC--- 58
QY 54 ASKNV-----LTTSEFYLSDCNVTSR-----CKYKLKSKTNTFCVTCENQ--APV 97
DB 59 FQKNVCKNGQSNVCYSNHNHTDCLTSSKYPNCYSRMSKGIIVACEGNPVVPV 118
QY 98 HF 99
DB 119 HF 120
RESULT 14
NRGPB
pancreatic ribonuclease (EC 3.1.27.5) - capybara
N:Alternate names: RNase A
C:Species: Hydrochaeris hydrochaeris (capybara, carpincho)
C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 29-Oct-1999
C:Accession: A00824
R:Beintema, J.J.; Neuteboom, B.
J. Mol. Evol. 19, 145-152, 1983
A:Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amir
A:Reference number: A92957; MUID:87036770; PMID:6571219
C:Accession: A00824
A:Molecule type: protein
A:Residues: 1-128 <BEI>
C:Superfamily: pancreatic ribonuclease

R;Bond, M.D.; Strydom, D.J.
Biochemistry 28, 6110-6113, 1989
A;Title: Amino acid sequence of bovine angiogenin.
A;Reference number: A32474; MUID:89375344; PMID:2775757
A;Accession: A32474
A;Molecule type: protein
A;Residues: 1-125 <BON>
A;Experimental source: plasma
R;Maes, P.; Damart, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartar, A.
FEBS Lett. 241, 41-45, 1988
A;Title: The complete amino acid sequence of bovine milk angiogenin.
A;Reference number: S02001; MUID:89065101; PMID:3197838
A;Accession: S02001
A;Molecule type: protein
A;Residues: 1-125 <MAE>
A;Experimental source: milk
R;Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
submitted to the Brookhaven Protein Data Bank, January 1995
A;Reference number: A65065; PDB:1AG1
A;Contents: annotation; X-ray crystallography, 1.5 angstroms, residues 1-125
R;Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995
A;Title: Crystal structure of bovine angiogenin at 1.5 Angstroms resolution.
A;Reference number: A58315; MUID:95224057; PMID:7708754
A;Contents: annotation; X-ray crystallography, 1.5 angstroms
R;Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
submitted to the Brookhaven Protein Data Bank, April 1996
A;Reference number: A65709; PDB:1GTO
A;Contents: annotation; Conformation by (1)H-NMR, residues 1-125
R;Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
Biochemistry 35, 8870-8880, 1996
A;Title: Solution structure of bovine angiogenin by (1)H nuclear magnetic resonance spectroscopy
A;Reference number: A58821; MUID:96280645; PMID:8688423
A;Contents: annotation; Conformation by (1)H-NMR
R;Reisdorf, C.; Abergeil, D.; Bontems, F.; Lallemand, J.Y.; Decottignies, J.P.; Spik, G.
Eur. J. Biochem. 224, 811-822, 1994
A;Title: Proton resonance assignments and secondary structure of bovine angiogenin.
A;Reference number: S48212; MUID:95010071; PMID:7925406
A;Contents: annotation; Conformation by (1)H-NMR
C;Function:
A;Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C;Superfamily: pancreatic ribonuclease
C;Keywords: angiogenesis; hydrolase; nucleic acid degradation
F;60-68/Region: receptor binding #status predicted
F;14, 41, 115/Active site: His, Lys, His #status predicted
F;27-82, 40-93, 58-108/Disulfide bonds: #status experimental
Query Match 22.0%; Score 128; DB 1; Length 125;
Best Local Similarity 34.0%; Pred. No. 8.2e-06;
Matches 33; Conservative 14; Mismatches 32; Indels 18; Gaps 5;
QY 17 DVDCCNNSTNLF--HCKDKNTFIYSRPPVKAICKGIIASKN-----VLTSEPYL 66
Db 24 DEYCFNMKNRLRTPCKDRNTTFHGNKNDKAICE-----DRNGQPYRGDLRIKSEFQI 79
QY 67 SDG---NVTSR-PCKYKLKKSNTFCVTCENQAPVHF 99
Db 80 TCKHKGSSAPPCKRYGATDSRVIVGCCGLPVHF 116
RESULT 8
NRCU
pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Myocastor coypus (nutria, coypu)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Accession: A00822
R;van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A;Reference number: A90612; MUID:77065676; PMID:999896
A;Accession: A00822
A;Molecule type: protein

A;Residues: 1-128 <VAN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12, 41, 119/Active site: His, Lys, His #status predicted
F;26-84, 40-95, 58-110, 65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 21.6%; Score 126; DB 1; Length 128;
Best Local Similarity 29.9%; Pred. No. 1.3e-05;
Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;
QY 7 FQKXHL-----TNRDVCNNIM-STNLF--HCKDKNTFIYSRPPVKAICKGIIASKNV 58
Db 8 FERQHMDSRGSPSTNPYCNEMKSRNMTQGRCKEPTVFVHEPLADVAVC-----FQKNV 63
QY 59 L-----TTSEFYLSDCNVTSRP-----CKYKLKKSNTFCVTCRNQ--APVHF 99
Db 64 LCKNGQTCYQSNMNHITDCRVTSNSDYPNCSYRTSQEKSIVVACENGPYPVHF 120
RESULT 9
NRWHK
pancreatic ribonuclease (EC 3.1.27.5) - minke whale
N;Alternate names: RNase 1; RNase A
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C;Accession: A00818
R;Jennens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A;Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease
A;Reference number: A00818; MUID:76277855; PMID:962870
A;Accession: A00818
A;Molecule type: protein
A;Residues: 1-124 <EMW>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12, 41, 119/Active site: His, Lys, His #status predicted
F;26-84, 40-95, 58-110, 65-72/Disulfide bonds: #status predicted
F;76/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 21.5%; Score 125; DB 1; Length 124;
Best Local Similarity 28.6%; Pred. No. 1.6e-05;
Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;
QY 5 LTFQKKHLTNRDVS-----CNNIMSTNLF--HCKDKNTFIYSRPPVKAICKGIIASK 56
Db 6 MKFQOHMDSGNSFGNNPNYCNQMMREKMTQGRCKPNTFVHESLEDVKAVC-----SQK 61
QY 57 NVL-----TTSEFYLSDCNVTSRP-----CKYKLKKSNTFCVTCENQ--APVHF 99
Db 62 NVLCKNGTNCYESNTWHITDCRQTGSSKYPNCAYKTSQKEKHIIIVACENGPYPVHF 120
RESULT 10
NRKS
pancreatic ribonuclease (EC 3.1.27.5) - casiragua
C;Species: Proechimys guairae (casiragua)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 30-Sep-1993
C;Accession: A00821
R;Beintema, J.J.; Knol, G.; Martena, B.
Biochim. Biophys. Acta 705, 102-110, 1982
A;Title: The primary structures of pancreatic ribonucleases from African porcupine and
A;Reference number: A90644; MUID:83000399; PMID:7115727
A;Accession: A00821
A;Molecule type: protein
A;Residues: 1-128 <BRI>
A;Note: residues 67-78 were positioned primarily by homology with other ribonucleases
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12, 41, 119/Active site: His, Lys, His #status predicted
F;26-84, 40-95, 58-110, 65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental

```

C:Species: Iguana iguana (common iguana)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C:Accession: S41111
R:Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Eur. J. Biochem. 219, 641-646, 1994
A:Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A:Reference number: S41111; MUID:94139745; PMID:8307028
A:Accession: S41111
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-119 <ZHA>
C:Superfamily: pancreatic ribonuclease

Query Match      24.7%; Score 144; DB 2; Length 119;
Best Local Similarity 30.1%; Pred.No. 1.9e-07;
Matches 34; Conservative 19; Mismatches 44; Indels 16; Gaps 5;

QY 3 DMLTFQKKHL-----TNRDVCNNIM---STNLFHCKDKNTFIYSRPEPVKAIC--KG 51
   |||:||||:
Db 2 DWSFQNKHIDYPENSASPNAYCDLMQRRNLNTKCKTRNTFVHASPEIQVCGSGG 61
   |||:||||:

QY 52 ITASKNVLTSP-FYLSDC----NVTSPCKYKLKSTNTFCVTCCENQAPVHF 99
   |: :||:||||:
Db 62 THYEDNLYDSNESFDTCKNWGGTAPSSCKYNGTGTGKRIRIACENQPVHF 114
   ||: :||:||||:

RESULT 6
NRUI
pancreatic ribonuclease (EC 3.1.27.5) - cuis
N:Alternate names: RNase 1; RNase A
C:Species: Galea musteloides (cuis)
C>Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 04-Oct-1996
C:Accession: A00827
R:Beintema, J.J.; Neuteboom, B.
J. Mol. Evol. 19, 145-152, 1983
A:Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amr
A:Reference number: A92957; MUID:87036770; PMID:6571219
A:Accession: A00827
A:Molecule type: protein
A:Residues: 1-124 <BEI>
A:Note: about one-third of the molecules lacked Ala-1
C:Comment: The cuis is a rodent belonging to the same subfamily as the guinea pig.
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,59-110,65-72/Disulfide bonds: #status predicted
F:94/Binding site: carboxylate (Asn) (covalent) #status absent

Query Match      22.7%; Score 132; DB 1; Length 124;
Best Local Similarity 30.6%; Pred.No. 3.2e-06;
Matches 38; Conservative 18; Mismatches 36; Indels 32; Gaps 7;

QY 2 SDLWTFQKKHL-----TNRDVCNNIM---STNLFHCKDKNTFIYSRPEPVKAICKG 51
   |||:||||:
Db 3 SCAMFQFQHMDSGDGHPNTN--YCNEMVRRSMTQGRCKPVNTFVHEPLEAVQAVC-- 58
   |||:||||:

QY 52 ITASKNV-----ITTSFYLSDCNVTSRP----CKYKLKSTNTFCVTCCEN--QA 95
   |||:||||:
Db 59 --SQKNVPCKNGQTNCYQSHSSMRITDCRVTSSSKYPNCSYRMTQAQKSIIVACEGTPSV 116
   |||:||||:

QY 96 PVHF 99
   |||||
Db 117 PVHF 120
   |||||

RESULT 7
A32474
angiogenin [validated] - bovine
N:Alternate names: angiogenesis factor
N:Contains: ribonuclease (EC 3.1.27.-)
C:Species: Bos primigenius taurus (cattle)
C>Date: 25-Sep-1989 #sequence_revision 25-Sep-1989 #text_change 15-Sep-2000
C:Accession: A32474; S02001; A30044; S48212

```

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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:38:36 ; Search time 9 5276 Seconds
(without alignments)
1060.090 Million cell updates/sec

Title: US-09-961-400-13

Perfect score: 582

Sequence: 1 MSDWLTQKHLNTRDVC.....TFCVTCENQAPVHFGVGHC 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 28366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	551	94.7	104	2 A39035	ribonuclease-relat
2	287	49.3	111	2 A27121	ribonuclease-relat
3	280.5	48.2	111	1 JX0120	ribonuclease-relat
4	264.5	45.4	111	2 JX0085	pancreatic ribonuc
5	144	24.7	119	2 S41111	pancreatic ribonuc
6	132	22.7	124	1 NRUI	pancreatic ribonuc
7	128	22.0	125	1 A32474	angiogenin [valida
8	126	21.6	128	1 NRUC	pancreatic ribonuc
9	125	21.5	124	1 NRHK	pancreatic ribonuc
10	120	20.6	128	1 NRKS	pancreatic ribonuc
11	120	20.6	128	1 NRGPB	pancreatic ribonuc
12	119.5	20.5	145	1 A35932	angiogenin precurs
13	118	20.3	124	1 NRCE	pancreatic ribonuc
14	117	20.1	128	1 NRYV	pancreatic ribonuc
15	116	19.9	125	1 B43825	pancreatic ribonuc
16	114	19.6	124	1 NRHP	angiogenin - rabbi
17	113	19.4	147	1 NRHDAG	pancreatic ribonuc
18	112	19.2	124	1 NRBOB	angiogenin precurs
19	112	19.2	124	1 NRPB	pancreatic ribonuc
20	112	19.2	128	1 NRPQ	pancreatic ribonuc
21	112	19.2	150	1 NRBO	pancreatic ribonuc
22	111.5	19.2	147	2 I52489	ribonuclease 4 (EC
23	111	19.1	124	2 S08549	ribonuclease - dom
24	111	19.1	128	1 NRHO	pancreatic ribonuc
25	111	19.1	167	2 S20066	pancreatic-type ri
26	110.5	19.0	123	1 A43825	angiogenin - pig
27	110.5	19.0	155	2 JG6159	eosinophil-associa
28	110	18.9	124	1 NKGPA	pancreatic ribonuc
29	110	18.9	156	2 JG6160	eosinophil-associa

30	109	18.7	124	1 NRSH	pancreatic ribonuc
31	109	18.7	124	1 NRPRH	pancreatic ribonuc
32	109	18.7	124	2 S07141	pancreatic ribonuc
33	108	18.6	124	1 NRWB	pancreatic ribonuc
34	108	18.6	124	1 NRGN	pancreatic ribonuc
35	107	18.4	124	1 NRGF	pancreatic ribonuc
36	105	18.0	124	1 NRDEO	pancreatic ribonuc
37	105	18.0	124	1 NRDM	pancreatic ribonuc
38	105	18.0	124	1 NRMM	pancreatic ribonuc
39	105	18.0	124	1 NRMB	pancreatic ribonuc
40	105	18.0	128	1 NROW2	pancreatic ribonuc
41	104	17.9	124	1 NRHY	pancreatic ribonuc
42	103	17.7	124	1 NRDER	pancreatic ribonuc
43	103	17.7	124	1 NRDEN	pancreatic ribonuc
44	103	17.7	124	1 NRKN	pancreatic ribonuc
45	102	17.5	124	1 NRDEF	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A39035

ribonuclease-related anti-tumor protein - northern leopard frog (fragment)

C:Species: Rana pipiens (northern leopard frog)

C>Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993

C:Accession: A39035

R:Ardelet, W.; Mikulski, S.M.; Shogen, K.

J. Biol. Chem. 266, 245-251, 1991

A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and ear

A:Reference number: A39035; MUID:91093131; PMID:1985896

A:Accession: A39035

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-104 <ARD>

C:Superfamily: pancreatic ribonuclease

Query Match 94.7%; Score 551; DB 2; Length 104;

Best Local Similarity 96.1%; Pred. No. 2.5e-48;

Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 DWTFFQKHLNTRDVCNINMTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLITS 62

DB 2 DWTFFQKHLNTRDVCNINMTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLITS 61

QY 63 EYILSDCNVTSRCPCKYKLSKSTNFCVTCENQAPVHFGVGHC 105

DB 62 EYILSDCNVTSRCPCKYKLSKSTNFCVTCENQAPVHFGVGSC 104

RESULT 2

A27121

ribonuclease-related sialic acid-binding lectin - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993

C:Accession: A27121

R:Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayanag

Biochemistry 26, 2189-2194, 1987

A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)

A:Reference number: A27121; MUID:87299649; PMID:3304421

A:Accession: A27121

A:Molecule type: protein

A:Residues: 1-111 <TIT>

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin

Query Match 49.3%; Score 287; DB 2; Length 111;

Best Local Similarity 49.1%; Pred. No. 8.1e-22;

Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 3 DWTFFQKHLNTRDVCNINMTNLF----HCKDKNTFIYSRPEPVKAICKGIASKNVLITS 58

DB 2 NWATFQKHLNTRDVCNINMTNLFIIYGVGQCKRVNTFIISATTVKAICTGVI-NMNV 60

Qy	1	MSDWLTFQKKHLTNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT	60
Db	1	MODWLTQKKHLTNTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT	60
Qy	61	TSEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC	105
Db	61	TFEYLSDCNVTSRPCKYKLLKSTITFCVTCENQAPVHFVGVGHC	105

Search completed: May 7, 2004, 21:51:57
Job time : 33.6904 secs

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; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
; FEATURE:
; OTHER INFORMATION: ribonuclease (RaPLR1)
US-09-948-391A-2

Query Match
Best Local Similarity 96.9%; Score 564; DB 10; Length 104;
Matches 102; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 DMLTFQKKHLTNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTS 62
DB 2 DMLTFQKKHLTNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTS 61

QY 63 EFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
DB 62 EFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 13
US-09-948-391A-4
; Sequence 4, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens
; OTHER INFORMATION: ribonuclease with Met23Leu substitution
; OTHER INFORMATION: (recombinant RaPLR1 Met23Leu)
US-09-948-391A-4

Query Match
Best Local Similarity 96.9%; Score 564; DB 10; Length 104;
Matches 101; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 DMLTFQKKHLTNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTS 62
DB 2 DMLTFQKKHLTNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTF 61

QY 63 EFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
DB 62 EFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 14
US-09-961-400-4
; Sequence 4, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
; US-09-961-400-4

Query Match
Best Local Similarity 96.9%; Score 564; DB 10; Length 104;
Matches 101; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 DMLTFQKKHLTNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTS 62
DB 2 DMLTFQKKHLTNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTF 61

QY 63 EFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
DB 62 EFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 15
US-09-948-391A-8
; Sequence 8, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens
; OTHER INFORMATION: ribonuclease with Met at position 1 and Met24Leu
; OTHER INFORMATION: substitution (recombinant Met(-1) RaPLR1 Met23Leu)
US-09-948-391A-8

Query Match
Best Local Similarity 96.2%; Score 560; DB 10; Length 105;
Matches 101; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy 63 EFYLSDCNVTSRPCKYKCLKKSTNTFCVTCENQAPVHFVGVGHC 105
62 EFYLSDCNVTSRPCKYKCLKKSTNTFCVTCENQAPVHFVGVGHC 104

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RESULT 9
US-09-948-391A-28
; Sequence 28, Application US/09948391A
; Publication No. US20030027311a1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Rana pipiens
; FEATURE:
; OTHER INFORMATION: Rana pipiens ribonuclease (RaPLR1) Clon
US-09-948-391A-28
; OTHER INFORMATION: Insert

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Query Match      98.5%; Score 573; DB 10; Length 127;
Best Local Similarity 100.0%; Pred.No. 5.1e-38;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DWLTFQKKHLTNTRDVDCNNIMSTNLPHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 62
Db 25 DWLTFQKKHLTNTRDVDCNNIMSTNLPHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 84

QY 63 EFYLSDCNVTSRPCKYKLLKKSTNFCVTCENQAPVHFVGVGHC 105
Db 85 EFYLSDCNVTSRPCKYKLLKKSTNFCVTCENQAPVHFVGVGHC 127

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RESULT 10
US-09-961-400-28
; Sequence 28, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 127
; TYPE: PRT
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; ORGANISM: Rana pipiens
US-09-961-400-28

Query Match          98.5%; Score 573; DB 10; Length 127;
Best Local Similarity 100.0%; Pred. NO. 5.1e-58;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWLTFQKKHLTNTRDVCNNIMSTNLPKCKDKNTFIYSRPEPVKAIKCKGIISKNNVLTT 62
Db 25 DWLTFQKKHLTNTRDVCNNIMSTNLPKCKDKNTFIYSRPEPVKAIKCKGIISKNNVLTT 84

Qy 63 EFLVSDCNVTSRCKYKIKKSTNTFCVTCENQAPVHFVGVGHC 105
Db 85 EFLVSDCNVTSRCKYKIKKSTNTFCVTCENQAPVHFVGVGHC 127

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RESULT 11
US-09-961-400-8
; Sequence 8, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-8

RESULT 12
US-09-948-391A-2
; Sequence 2, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641

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; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with Gln1ser substitution
; OTHER INFORMATION: (recombinant RaPRL1 Q1S)
US-09-948-391A-11

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Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SDWLTFOKKHLTNTTRDVCNNIMSTNLFHCKDKNTFYISRPVPVKAICKGIIASKNVLT 61
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QY 62 SEFYLSDCNVTSRPCKYKLLKSKTNTFCVTCENQAPVHFVGVGHC 105
DB 61 SEFYLSDCNVTSRPCKYKLLKSKTNTFCVTCENQAPVHFVGVGHC 104

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US-09-961-400-11
; Sequence 11, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-11

Query Match          99.1%; Score 577; DB 10; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SDWLTFOKKHLTNTTRDVCNNIMSTNLFHCKDKNTFYISRPVPVKAICKGIIASKNVLT 61
DB 1 SDWLTFOKKHLTNTTRDVCNNIMSTNLFHCKDKNTFYISRPVPVKAICKGIIASKNVLT 60

QY 62 SEFYLSDCNVTSRPCKYKLLKSKTNTFCVTCENQAPVHFVGVGHC 105
DB 61 SEFYLSDCNVTSRPCKYKLLKSKTNTFCVTCENQAPVHFVGVGHC 104

RESULT 7
US-09-961-400-9
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; Sequence 9, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-9
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Best Local Similarity 98.1%; Pred. No. 2.6e-58;
Matches 103; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSDWLTFOKKHLTNTTRDVCNNIMSTNLFHCKDKNTFYISRPVPVKAICKGIIASKNVLT 60
DB 7 MQDWLTFOKKHLTNTTRDVCNNILSTNLFHCKDKNTFYISRPVPVKAICKGIIASKNVLT 66

QY 61 TSEFYLSDCNVTSRPCKYKLLKSKTNTFCVTCENQAPVHFVGVGHC 105
DB 67 TSEFYLSDCNVTSRPCKYKLLKSKTNTFCVTCENQAPVHFVGVGHC 111
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RESULT 8
US-09-961-400-2
; Sequence 2, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; NUMBER OF SEQ ID NOS: 43
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; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-2
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Query Match          98.5%; Score 573; DB 10; Length 104;
Best Local Similarity 100.0%; Pred. No. 4e-58;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 13, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 13
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-13

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Best Local Similarity 100.0%; Pred. No. 3.7e-59;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TSEFVLSDCNVTSPCKYKLLKSTNTFCVTCEQAHPVHVGHC 105
Db 61 TSEFVLSDCNVTSPCKYKLLKSTNTFCVTCEQAHPVHVGHC 105

RESULT 3
US-09-948-391A-6
; Sequence 6, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens
; OTHER INFORMATION: ribonuclease with Met at position 1 (recombinant)
; OTHER INFORMATION: Met (-1) RALRL1
US-09-948-391A-6

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Best Local Similarity 99.0%; Pred. No. 1.1e-58;
Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 61 TSEFVLSDCNVTSPCKYKLLKSTNTFCVTCEQAHPVHVGHC 105

RESULT 4
US-09-961-400-6
; Sequence 6, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-6

Query Match 99.3%; Score 578; DB 10; Length 105;
Best Local Similarity 99.0%; Pred. No. 1.1e-58;
Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; Sequence 11, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:40 ; Search time 33.6904 Seconds
(without alignments)
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Title: US-09-961-400-13

Perfect score: 582

Sequence: 1 MSDWLTQKKHLNTRDVC.....TFCVTCENQAPVHFVGVC 105

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	582	100.0	105	US-09-948-391A-13	Sequence 13, Appl
2	582	100.0	105	US-09-961-400-13	Sequence 13, Appl
3	578	99.3	105	US-09-948-391A-6	Sequence 6, Appl
4	578	99.3	105	US-09-961-400-6	Sequence 6, Appl
5	577	99.1	104	US-09-948-391A-11	Sequence 11, Appl
6	577	99.1	104	US-09-961-400-11	Sequence 11, Appl
7	575	98.8	111	US-09-961-400-9	Sequence 9, Appl
8	573	98.5	104	US-09-961-400-2	Sequence 2, Appl
9	573	98.5	127	US-09-948-391A-28	Sequence 28, Appl
10	573	98.5	127	US-09-961-400-28	Sequence 28, Appl
11	565	97.1	105	US-09-961-400-8	Sequence 8, Appl
12	564	96.9	104	US-09-948-391A-2	Sequence 2, Appl
13	564	96.9	104	US-09-948-391A-4	Sequence 4, Appl
14	564	96.9	104	US-09-961-400-4	Sequence 4, Appl
15	560	96.2	105	US-09-948-391A-8	Sequence 8, Appl

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16 560 96.2 111 10 US-09-948-391A-9
17 556 95.5 105 14 US-10-153-882-2
18 551 94.7 104 9 US-09-986-119-1
19 551 94.7 104 10 US-09-918-887-1
20 543 93.3 104 12 US-10-461-713-53
21 445 76.5 83 9 US-09-986-119-3
22 445 76.5 83 10 US-09-918-887-3
23 285.5 49.1 111 10 US-09-948-391A-26
24 285.5 49.1 111 10 US-09-961-400-26
25 281.5 48.4 111 10 US-09-961-400-17
26 280.5 48.2 110 10 US-09-948-391A-24
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36 266.5 45.8 110 10 US-09-948-391A-19
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39 144 24.7 119 15 US-10-074-978A-139
40 128.5 22.1 124 13 US-10-016-447-5
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42 113 19.4 147 9 US-09-286-240-6
43 113 19.4 147 9 US-09-863-777-2
44 113 19.4 147 9 US-09-731-872-254
45 113 19.4 147 10 US-09-876-997-254

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ALIGNMENTS

RESULT 1

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US-09-948-391A-13
; Sequence 13, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: Ribonuclease with Met at position 1 and Gln2Ser
; OTHER INFORMATION: substitution (recombinant Met(-1) RapLR1 Q1S)
US-09-948-391A-13

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Query Match 100.0%; Score 582; DB 10; Length 105;

Best Local Similarity 100.0%; Pred. No. 3.7e-59;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDWLTQKKHLNTRDVCNNIMSTNLFCKCKNTFYSRPEFVKAIKGIASKNVL 60

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; TELEX: No. 5728805 Applicable
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
; DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-1

Query Match 94.7%; Score 551; DB 1; Length 104;
Best Local Similarity 96.1%; Pred. No. 1.5e-59;
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DB 2 DWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEVPVKAICKGIIRASKNVLTTTS 61
QY 63 EYLSDCNVTSPCKYKIKKSTNTFCVTCENQAPVHFVGVC 105
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Search completed: May 7, 2004, 21:40:44
Job time : 12.1796 secs

;/ FILING DATE: 13-NOV-1989
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Jay, Mark H.
;/ REGISTRATION NUMBER: 27507
;/ REFERENCE/DOCKET NUMBER: 5006 US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 718-625-0399
;/ TELEFAX: 718-625-0399
;/ TELEX: No. 5529775 Applicable
;/ INFORMATION FOR SEQ ID NO: 1:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 104 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ HYPOTHETICAL: N
;/ ANTI-SENSE: N
;/ FRAGMENT TYPE: N-terminal
;/ ORIGINAL SOURCE:
;/ ORGANISM: Rana pipiens
;/ DEVELOPMENTAL STAGE: Embryo
;/ US-08-283-971-1

Query Match 94.7%; Score 551; DB 1; Length 104;
Best Local Similarity 96.1%; Pred. No. 1.5e-59;
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 DLTFTQKKHLNTRDVCNINMSTNLFHCKDKNTFYSRPEPVKAICKGIASKNVLTTS 62
Db 2 DLTFTQKKHLNTRDVCNINMSTNLFHCKDKNTFYSRPEPVKAICKGIASKNVLTTS 61

QY 63 EFLSDCNVTSRCPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 105
Db 62 EFLSDCNVTSRCPCKYKLLKSTNFCVTCENQAPVHFVGVGSC 104

RESULT 14

;/ Sequence 1, Application US/07921619
;/ Patent No. 5595734
;/ GENERAL INFORMATION:
;/ APPLICANT: Ardelt Ph.D, Wojciech J.
;/ APPLICANT: Mikulski, Stanislaw M.
;/ TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
;/ NUMBER OF SEQUENCES: 1
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Mark H. Jay, P.C.
;/ STREET: P.O. Box 020083, General Post Office
;/ CITY: Brooklyn
;/ STATE: New York
;/ COUNTRY: USA
;/ ZIP: 11202-0002
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.24
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/07/921,619
;/ FILING DATE: 19920728
;/ CLASSIFICATION: 530
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/178,118
;/ FILING DATE: 06-APR-1988
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/436,141
;/ FILING DATE: 13-NOV-1989
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Jay, Mark H.
;/ REGISTRATION NUMBER: 27507
;/ REFERENCE/DOCKET NUMBER: 5005 US
;/ TELECOMMUNICATION INFORMATION:

;/ TELEPHONE: 718-625-0399
;/ TELEFAX: 718-625-0399
;/ TELEX: No. 5595734 Applicable
;/ INFORMATION FOR SEQ ID NO: 1:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 104 amino acids
;/ TYPE: AMINO ACID
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ HYPOTHETICAL: N
;/ ANTI-SENSE: N
;/ FRAGMENT TYPE: N-terminal
;/ ORIGINAL SOURCE:
;/ ORGANISM: Rana pipiens
;/ DEVELOPMENTAL STAGE: Embryo
;/ US-07-921-619-1

Query Match 94.7%; Score 551; DB 1; Length 104;
Best Local Similarity 96.1%; Pred. No. 1.5e-59;
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 DLTFTQKKHLNTRDVCNINMSTNLFHCKDKNTFYSRPEPVKAICKGIASKNVLTTS 62
Db 2 DLTFTQKKHLNTRDVCNINMSTNLFHCKDKNTFYSRPEPVKAICKGIASKNVLTTS 61

QY 63 EFLSDCNVTSRCPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 105
Db 62 EFLSDCNVTSRCPCKYKLLKSTNFCVTCENQAPVHFVGVGSC 104

RESULT 15

;/ US-08-467-955-1
;/ Sequence 1, Application US/08467955
;/ Patent No. 5728805
;/ GENERAL INFORMATION:
;/ APPLICANT: Ardelt Ph.D, Wojciech J.
;/ TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
;/ NUMBER OF SEQUENCES: 2
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Mark H. Jay, P.A.
;/ STREET: P.O. Box E
;/ CITY: Short Hills
;/ STATE: New Jersey
;/ COUNTRY: USA
;/ ZIP: 07078-0383
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.24
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/467,955
;/ FILING DATE:
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/178,118
;/ FILING DATE: 06-APR-1988
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/436,141
;/ FILING DATE: 13-NOV-1989
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/814,332
;/ FILING DATE: 03-FEB-1992
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/283,970
;/ FILING DATE: 01-AUG-1994
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Jay, Mark H.
;/ REGISTRATION NUMBER: 27507
;/ REFERENCE/DOCKET NUMBER: 5007 US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 201-912-9066

APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 41,739
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-51

Query Match 95.5%; Score 556; DB 3; Length 358;
Best Local Similarity 95.2%; Pred. No. 1.9e-59;
Matches 100; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 MSDWLTFOKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLT 60
DB 1 MEDWLTFOKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLT 60
QY 61 TSEFYLSDCNVTSPCKYKLLKSTNTFCVTENQAPVHFVGVGHC 105
DB 61 TSEFYLSDCNVTSPCKYKLLKSTNTFCVTENQAPVHFVGVGSC 105

RESULT 12
US-08-875-811-26
Sequence 26, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluís
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-26

Query Match 95.4%; Score 555; DB 3; Length 105;
Best Local Similarity 95.2%; Pred. No. 5e-60;
Matches 100; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 MSDWLTFOKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLT 60
DB 1 MSDWLTFOKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLT 60
QY 61 TSEFYLSDCNVTSPCKYKLLKSTNTFCVTENQAPVHFVGVGHC 105
DB 61 TSEFYLSDCNVTSPCKYKLLKSTNTFCVTENQAPVHFVGVGSC 105

RESULT 13
US-08-283-971-1
Sequence 1, Application US/08283971
Patent No. 5529775
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,971
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/921,180
FILING DATE: 30-JUL-1992
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141

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; DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-2

Query Match          95.5%; Score 556; DB 1; Length 104;
Best Local Similarity 97.1%; Pred. No. 3.7e-60;
Matches 100; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 DMLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLTTS 62
Db 2 DMLTFQKKHVTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLTTS 61

QY 63 EYFLSDCNVTSRPPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 62 EYFLSDCNVTSRPPCKYKLLKSTNFKVTCENQAPVHFVGVGSC 104

RESULT 9
US-08-875-811-39
; Sequence 39, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-39

Query Match          95.5%; Score 556; DB 3; Length 105;
Best Local Similarity 95.2%; Pred. No. 3.8e-60;
Matches 100; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSDWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60
Db 1 MEDWLTFQKKHINTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60

QY 61 TSEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
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Db 61 TSEFYLSDCNVTSRPCKYKLLKSTNFKVTCENQAPVHFVGVGSC 105

RESULT 10
US-08-875-811-41
; Sequence 41, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-41

Query Match          95.5%; Score 556; DB 3; Length 355;
Best Local Similarity 95.2%; Pred. No. 1.8e-59;
Matches 100; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSDWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60
Db 251 MEDWLTFQKKHINTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 310

QY 61 TSEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 311 TSEFYLSDCNVTSRPCKYKLLKSTNFKVTCENQAPVHFVGVGSC 355

RESULT 11
US-08-875-811-51
; Sequence 51, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
```

```
/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 64:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 355 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Protein
/ LOCATION: 1..355
/ OTHER INFORMATION: /note= "E6FB[Met-(-1)]SerrOnc"
US-08-875-811-64

Query Match 96.2%; Score 560; DB 3; Length 355;
Best Local Similarity 96.2%; Pred. No. 6e-60;
Matches 101; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSPPEPVKAICKGIIASKNVLT 60
Db 251 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSPPEPVKAICKGIIASKNVLT 310

Qy 61 TSEFYSLDCNVTSPCKYKLLKSKSTNTFCVTCENQAPVHFVGVGHC 105
Db 311 TSEFYSLDCNVTSPCKYKLLKSKSTNTFCVTCENQAPVHFVGVGSC 355

RESULT 7
US-08-875-811-55
; Sequence 55, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Luis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 amino acids
; TYPE: amino acid
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/
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-875-811-55

Query Match 96.2%; Score 560; DB 3; Length 366;
Best Local Similarity 96.2%; Pred. No. 6.2e-60;
Matches 101; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSPPEPVKAICKGIIASKNVLT 60
Db 262 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSPPEPVKAICKGIIASKNVLT 321

Qy 61 TSEFYSLDCNVTSPCKYKLLKSKSTNTFCVTCENQAPVHFVGVGHC 105
Db 322 TSEFYSLDCNVTSPCKYKLLKSKSTNTFCVTCENQAPVHFVGVGSC 366

RESULT 8
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D, Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; TELEX: No. 5728805 Applicable
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
```

STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-49

Query Match 96.2%; Score 560; DB 3; Length 355;
Best Local Similarity 96.2%; Pred. No. 6e-60;
Matches 101; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSDWLTQKKHLTNRDVCNNIMSTNLFHCKDKNTFYSPPEPVKAICKGIASKNVLT 60
DB 251 MSDWLTQKKHLTNRDVCNNIMSTNLFHCKDKNTFYSPPEPVKAICKGIASKNVLT 310
QY 61 TSEYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
DB 311 TSEYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 355

RESULT 5
US-08-875-811-57
Sequence 57, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811

FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-57

Query Match 96.2%; Score 560; DB 3; Length 355;
Best Local Similarity 96.2%; Pred. No. 6e-60;
Matches 101; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSDWLTQKKHLTNRDVCNNIMSTNLFHCKDKNTFYSPPEPVKAICKGIASKNVLT 60
DB 1 MSDWLTQKKHLTNRDVCNNIMSTNLFHCKDKNTFYSPPEPVKAICKGIASKNVLT 60
QY 61 TSEYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
DB 61 TSEYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 105

RESULT 6
US-08-875-811-64
Sequence 64, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US

Matches 101; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSPRPVKAICKGIIASKNVLT 60
Db 8 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSPRPVKAICKGIIASKNVLT 67
Qy 61 TSEFYSDCNVTSRPCKYKLLKSKSTNTFCVTCENQAPVHFVGVGHC 105
Db 68 TSEFYSDCNVTSRPCKYKLLKSKSTNTFCVTCENQAPVHFVGVGSC 112

RESULT 2

US-08-875-811-59

; Sequence 59, Application US/08875811

; Patent No. 6045793

; GENERAL INFORMATION:

; APPLICANT: Rybak, Susanna M.

; APPLICANT: Newton, Dianne L.

; APPLICANT: Boque, Lluís

; APPLICANT: Wlodawer, Alexander

; TITLE OF INVENTION: Recombinant Ribonuclease Proteins

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/875,811

; FILING DATE: 19-FEB-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/02588

; FILING DATE: 19-FEB-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/011,800

; FILING DATE: 21-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Paris, Susan K.

; REGISTRATION NUMBER: 41,739

; REFERENCE/DOCKET NUMBER: 015280-244100US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 251 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-875-811-59

Query Match

Best Local Similarity 96.2%; Score 560; DB 3; Length 251;

Matches 101; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSPRPVKAICKGIIASKNVLT 60
Db 147 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSPRPVKAICKGIIASKNVLT 206

Qy 61 TSEFYSDCNVTSRPCKYKLLKSKSTNTFCVTCENQAPVHFVGVGHC 105

Db 207 TSEFYSDCNVTSRPCKYKLLKSKSTNTFCVTCENQAPVHFVGVGSC 251

RESULT 3

US-08-875-811-61

; Sequence 61, Application US/08875811

; Patent No. 6045793

; GENERAL INFORMATION:

; APPLICANT: Rybak, Susanna M.

; APPLICANT: Newton, Dianne L.

; APPLICANT: Boque, Lluís

; APPLICANT: Wlodawer, Alexander

; TITLE OF INVENTION: Recombinant Ribonuclease Proteins

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/875,811

; FILING DATE: 19-FEB-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/02588

; FILING DATE: 19-FEB-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/011,800

; FILING DATE: 21-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Paris, Susan K.

; REGISTRATION NUMBER: 41,739

; REFERENCE/DOCKET NUMBER: 015280-244100US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 61:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 254 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-875-811-61

Query Match

Best Local Similarity 96.2%; Score 560; DB 3; Length 254;

Matches 101; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db 1 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSPRPVKAICKGIIASKNVLT 60

Qy 61 TSEFYSDCNVTSRPCKYKLLKSKSTNTFCVTCENQAPVHFVGVGHC 105

Db 61 TSEFYSDCNVTSRPCKYKLLKSKSTNTFCVTCENQAPVHFVGVGSC 105

RESULT 4

US-08-875-811-49

; Sequence 49, Application US/08875811

; Patent No. 6045793

; GENERAL INFORMATION:

; APPLICANT: Rybak, Susanna M.

; APPLICANT: Newton, Dianne L.

; APPLICANT: Boque, Lluís

; APPLICANT: Wlodawer, Alexander

; TITLE OF INVENTION: Recombinant Ribonuclease Proteins

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:28:45 ; Search time 12.1796 Seconds
(without alignments)
445.066 Million cell updates/sec

Title: US-09-961-400-13
Perfect score: 582
Sequence: 1 MSDWLFQKGLNTRDVC.....TFVCVCNQAPVHFVGVGHC 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	560	96.2	112	3	US-08-875-811-32
2	560	96.2	251	3	US-08-875-811-59
3	560	96.2	254	3	US-08-875-811-61
4	560	96.2	355	3	US-08-875-811-49
5	560	96.2	355	3	US-08-875-811-57
6	560	96.2	355	3	US-08-875-811-64
7	560	96.2	366	3	US-08-875-811-55
8	556	95.5	104	1	US-08-467-955-2
9	556	95.5	105	3	US-08-875-811-39
10	556	95.5	355	3	US-08-875-811-41
11	556	95.5	358	3	US-08-875-811-51
12	555	95.4	105	3	US-08-875-811-26
13	551	94.7	104	1	US-08-283-971-1
14	551	94.7	104	1	US-07-921-619-1
15	551	94.7	104	1	US-08-467-955-1
16	551	94.7	104	2	US-08-891-848-13
17	551	94.7	104	3	US-08-875-811-1
18	551	94.7	104	3	US-09-394-268-1
19	551	94.7	104	4	US-09-071-672-1
20	551	94.7	104	4	US-09-687-748-1
21	551	94.7	104	4	US-08-626-288-1
22	551	94.7	104	4	US-09-095-429-1
23	551	94.7	104	4	US-09-986-119-1
24	551	94.7	106	3	US-08-875-811-28
25	551	94.7	107	3	US-08-875-811-30
26	551	94.7	129	3	US-08-875-811-63
27	551	94.7	358	3	US-08-875-811-45

28 551 94.7 365 3 US-08-875-811-53
29 551 94.7 379 3 US-08-875-811-43
30 549 94.3 105 3 US-08-875-811-24
31 548 94.2 104 4 US-08-626-288-2
32 548 94.2 104 4 US-09-095-429-2
33 543 93.3 104 3 US-09-394-268-2
34 543 93.3 104 4 US-09-687-748-2
35 532 91.4 107 3 US-08-875-811-20
36 499 85.7 360 3 US-08-875-811-47
37 484.5 83.2 111 3 US-08-875-811-22
38 445 76.5 83 4 US-08-875-811-2
39 445 76.5 83 4 US-09-071-672-3
40 445 76.5 83 4 US-09-986-119-3
41 287 49.3 111 2 US-08-851-848-12
42 287 49.3 111 3 US-08-875-811-8
43 216.5 37.2 114 3 US-09-223-118-4
44 204.5 35.1 114 3 US-09-223-118-2
45 203.5 35.0 114 3 US-09-223-118-1

ALIGNMENTS

RESULT 1
US-08-875-811-32
; Sequence 32, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-32

Query Match 96.2%; Score 560; DB 3; Length 112;
Best Local Similarity 96.2%; Pred. No. 1.3e-60;

Search completed: May 11, 2004, 14:35:05
Job time : 11.0452 secs

ID	RNBP_AX1PR	STANDARD;	PRT;	151 AA.
AC	P87350;			
AC	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DT	Ribonuclease, brain (EC 3.1.27.-) (BRB).			
GN	BRN.			
OS	Axis porcinus (Hog deer).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;			
OC	Cervidae; Cervinae; Axis.			
OX	NCBI_TaxID=57737;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=98278842; PubMed=9611269;			
RX	Breukelman H.J.; van der Munnik N.; Kleineidam R.G.; Furia A.,			
RA	Beintema J.J.;			
RA	"Secretory ribonuclease genes and pseudogenes in true ruminants.";			
RL	Gene 212:259-268 (1998).			
RT	CC			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.			
CC	CC			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; Y11670; CAA72368.1; -.			
CC	HSSP; P00656; ISRN.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; rnasea; 1.			
DR	PRINTS: PR00794; RIBONUCLEASE.			
DR	ProDom; PD000535; RNaseA; 1.			
DR	SMART; SM00092; RNase_Pc; 1.			
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.			
DR	Hydrolase; Nuclease; Endonuclease; Glycoprotein.			
KW	ACT_SITE 41 41			
FT	DISULFID 26 84			
FT	DISULFID 40 95			
FT	DISULFID 58 110			
FT	DISULFID 65 72			
FT	CARBOHYD 62 62			
FT	CARBOHYD 129 129			
FT	CARBOHYD 133 133			
FT	SEQUENCE 151 AA; 16819 MW; E95F3757FFC5B233 CRC64;			
SEQ				
Query Match				
Best Local Similarity 21.0%; Score 127.5; DB 1; Length 151;				
Matches 37; Conservative 17; Mismatches 44; Indels 23; Gaps 7;				
QY	5	ATFOQRKH-----INTPIICNTIMDNNIYVGGCKRVNTEFISSATTTKAICTGVINM 58		
Db	6	AKPRRHM DAGSSSGNSVNCNMKRR-RWTGRCCKPVMFTVHESLDSVKAVCS---QK 61		
QY	59	NVL-----STTRFOLNCTRTSITPRP-CPYSSRRTETNYICVKE-NQY-PVHFA 105		
Db	62	NITCKNGQPCVQSNSTMNITDCRETGSSKYPNCAYKTSQKQYKIVACEGNPVVPVHFD 121		
QY	106	G 106		
Db	122	G 122		
RESULT 15				
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ID	RNP_IGUIG	STANDARD;	PRT;	119 AA.
AC	P80287;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			

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SQ SEQUENCE 124 AA; 13804 MW; 0AC28CDE14111845 CRC64;
Query Match 21.9%; Score 132.5; DB 1; Length 124;
Best Local Similarity 31.6%; Pred. No. 26-07; Indels 17; Gaps 6;
Matches 36; Conservative 19; Mismatches 42;

QY 7 FQKHII-----INTPIICNTIMDNIIYVGGCKRVNTFIISATTVKAICTGV-INNM 59
Db 8 FQKHMDPSSSSNSNCLMWSRR-NMTQGRCKPVNTFVHESLADVQAVCSQINVCCK 66

QY 60 VLSTTRFQINT-----CTRISITPRP-CPYSSRTETNYICVKCNQ--YPVHF 104
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RESULT 11
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AC P79351;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
OS Capreolus capreolus (Roe deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Odocoileinae; Capreolus.
OX NCBI_TaxID=9858;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98278842; PubMed=9611269;
RA Breukelman H.J., van der Munnik N., Kleiheidam R.G., Furia A.,
RA Beintema J.J.;
RT "Secretory ribonuclease genes and pseudogenes in true ruminants.";
RL Gene 212:259-268(1998).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y11673; CAAT7371.1; -.
DR HSSP; P00656; 1SRN.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; xnaaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease; Glycoprotein.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 41 84 BY SIMILARITY.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
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FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 151 AA; 16971 MW; 392D0E6302F006A6 CRC64;

Query Match 21.2%; Score 128.5; DB 1; Length 151;
Best Local Similarity 29.4%; Pred. No. 6.6e-07;
Matches 35; Conservative 17; Mismatches 44; Indels 23; Gaps 6;

QY 5 ATFOQKHII-----INTPIICNTIMDNIIYVGGCKRVNTFIISATTVKAICTGVINM 58
Db 6 AKFRQHMDSGSSSGNPNYCNQMRR-RMTHGRCKPVNTFVHESLDNVRKAVCS---QK 61

SQ SEQUENCE 124 AA; 13804 MW; 0AC28CDE14111845 CRC64;
Query Match 21.9%; Score 132.5; DB 1; Length 124;
Best Local Similarity 31.6%; Pred. No. 26-07; Indels 17; Gaps 6;
Matches 36; Conservative 19; Mismatches 42;

QY 7 FQKHII-----INTPIICNTIMDNIIYVGGCKRVNTFIISATTVKAICTGV-INNM 59
Db 8 FQKHMDPSSSSNSNCLMWSRR-NMTQGRCKPVNTFVHESLADVQAVCSQINVCCK 66

QY 60 VLSTTRFQINT-----CTRISITPRP-CPYSSRTETNYICVKCNQ--YPVHF 104
Db 67 NGQTNCYQSNSTMTITDCRQTGSSKYPNCAYKASQEQKHIIIVACEGDPVPVHF 120

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AC P80929;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin-2 (EC 3.1.27.-).
GN ANG2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovioidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX TISSUE=Milk, and Serum;
RX MEDLINE=97409980; PubMed=9266695;
RA Striydom D.J., Bond M.D., Vallee B.L.;
RT "An angiogenic protein from bovine serum and milk -- purification and
RT primary structure of angiogenin-2.";
RL Eur. J. Biochem. 247:535-544(1997).
CC -!- FUNCTION: Binds tightly to placental ribonuclease inhibitor and
CC has very low ribonuclease activity. Has potent angiogenic
CC activity. Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs.
CC -!- TISSUE SPECIFICITY: Serum and milk.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC HSSP; P10152; IAGI.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; xnaaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Glycoprotein;
KW Pyrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 39 39 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.
FT DISULFID 25 80 BY SIMILARITY.
FT DISULFID 38 91 BY SIMILARITY.
FT DISULFID 56 106 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC...).
SQ SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;

Query Match 21.0%; Score 127.5; DB 1; Length 123;
Best Local Similarity 30.6%; Pred. No. 6.8e-07;
Matches 33; Conservative 19; Mismatches 43; Indels 13; Gaps 5;

QY 7 FQKHIIINTPI-----ICNTIMDNIIYVGGCKRVNTFIISATTVKAIC---TCVINM 58
Db 8 FLRKHYDFSPGTGHDDRYCNTMMERR--NMTRECKDTNTIHGNSDDIRACDDRNGEYR 65

QY 59 NVLSTTR--FQNTCTRTSITPR-CPYSSRTETNYICVKCNQYVPH 103
Db 66 NGLRSRSPFQVTTCHRGSGSPRCRYAFRANRVIIRCDDGPFH 113

RESULT 13
RNRB_GIRCA STANDARD; PRT; 141 AA.
AC Q29542; Q29533;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
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Query Match	22.0%;	Score 133.5;	DB 1;	Length 167;
Best Local Similarity	31.4%;	Pred. No. 2.1e-07;		

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DR PIR; A00818; NRWEK.
DR HSSP; P00656; 1SRN.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase P; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 76 76 N-LINKED (GUCNAC...) (30%).
SQ SEQUENCE 124 AA; 14125 MW; F5745459F697E20 CRC64;

Query Match 22.4%; Score 135.5; DB 1; Length 124;
Best Local Similarity 33.3%; Pred. No. 9.4e-08;
Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

QY 7 FQKHII-----NPIIONTMDNNIYVGGCKRVNTPFISSATTVAICTGVINMV 60
Db 8 FQKHMDSGNSPNNPNYCNQMMRR-KMTQGRCKPVNTFVHESLEDVKA VCS---QKNV 63
QY 61 I-----STTRFQNTCTRTSITPRP-CPYSSRTETNYCVKCE-NQY-PVHF 104
Db 64 LCKNGRTCYESNSTMHTDCRQTGSSKYPNCAYKTSQKEKHIVACEGNYPVPVHF 120

RESULT 8
ANGI_MOUSE STANDARD; PRT; 145 AA.
ID ANGI_MOUSE STANDARD; PRT; 145 AA.
AC P21570;
DC 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91025023; PubMed=2222458;
RA Bond M.D., Vallee B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length

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RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP PARTIAL SEQUENCE.
RC TISSUE=Serum;
RX MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
RT angiogenins: discernment of functionally important residues and
RT regions.";
RL Biochim. Biophys. Acta 1162:177-186 (1993).
CC -!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
CC to act on the surface of endothelial cells; once bound,
CC angiogenin is endocytosed and translocated to the nucleus, thereby
CC promoting the endothelial invasiveness necessary for blood vessel
CC formation. Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
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CC
CC EMBL; U22516; AAA91366.1; -.
CC EMBL; BC055355; AAH55355.1; -.
CC PIR; A35932; A35932.
CC HSSP; P03950; 1A4Y.
CC MGD; MGI:88022; Ang.
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; RNaseA; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
CC ProDom; PD000535; RNaseA; 1.
CC SMART; SM00092; RNase P; 1.
CC PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal; Pyroliidone carboxylic acid.
FT CHAIN 1 24
FT SIGNAL 25 145
FT MOD_RES 25 25 ANGIOGENIN.
FT PYROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT ACT_SITE 137 137 BY SIMILARITY.
FT DISULFID 50 104 BY SIMILARITY.
FT DISULFID 63 115 BY SIMILARITY.
FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA; 16228 MW; 06944260BB764938 CRC64;

Query Match 22.4%; Score 135.5; DB 1; Length 145;
Best Local Similarity 39.5%; Pred. No. 1.1e-07;
Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3;

QY 34 CKRWTFPISSATTVAICTGVINMV-ISTTRFQNTCTRTSITPR-PCPYSSRTE 88
Db 63 CKDWTFPIHGNKAIKAGANGSPYRENLRMSKSPFQVTTCKTGSPRPCCQYRASAG 122
QY 89 TNYVCVKCNQXPVHF 104
Db 123 FRHVIACENGLPVHF 138

RESULT 9
RNRB_BOVIN STANDARD; PRT; 167 AA.
ID RNRB_BOVIN STANDARD; PRT; 167 AA.
AC P39873;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)

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RT RT fibroblasts."
RL Mol. Cell. Biol. 17:1503-1512(1997).
CC -!- FUNCTION: Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs (By similarity).
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U22519; AAA91367.1; -.
DR HSP; P03950; IAGI.
DR MGD; MGI:104984; Angip.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
SQ SEQUENCE 145 AA; 16696 MW; 16962 MW; DE9D3BC92F1D682C CRC64;
Query Match 25.5%; Score 154.5; DB 1; Length 145;
Best Local Similarity 43.6%; Pred. No. 1e-09;
Matches 34; Conservative 12; Mismatches 23; Indels 9; Gaps 4;
QY 34 CKRVNFIISATTVKAIC-----TGVINNVLTTRFQNTCTRTSITPR-PCPYSSR 86
Db 63 CKEVNFIHDTKKNKAICGNGRPGYV-NPRI-SNSRFQVTTCTHKGSPRPCCYNAF 120
QY 87 TETNYICVKCENQYVPHF 104
Db 121 KQFYIVVACEDGWPVHF 138
RESULT 6
ID_ANGR_MOUSE STANDARD; PRT; 145 AA.
AC Q64438;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin-related protein precursor.
DE ANGRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Liver;
RX MEDLINE=96079109; PubMed=8530072;
RA Brown W.E., Nobile V., Subramanian V., Shapiro R.;
RT "The mouse angiogenin gene family: structures of an angiogenin-related
RT protein gene and two pseudogenes."
RL Genomics 29:200-206(1995).
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U22519; AAA91367.1; -.
DR HSP; P03950; IAGI.
DR MGD; MGI:104984; Angip.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429C4D CRC64;
Query Match 24.7%; Score 149.5; DB 1; Length 145;
Best Local Similarity 43.4%; Pred. No. 3.5e-09;
Matches 33; Conservative 10; Mismatches 28; Indels 5; Gaps 3;
QY 34 CKRVNFIISATTVKAIC--TGVINNV-LSTRFQNTCTRTSITPR-PCPYSSRTE 88
Db 63 CKDVTFIHDTKKNKAICGKSPYGRNLRISKRQVTTCTHKGSPRPCCYRASKG 122
QY 89 TNYICVKCENQYVPHF 104
Db 123 FRYIIIGCENGWPVHF 138
RESULT 7
ID_RNP_BALAC STANDARD; PRT; 124 AA.
AC P00673;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
DE RNASE1 OR RNS1.
OS Balaenoptera acutorostrata (Minke whale) (lesser rorqual).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaenopteridae; Balaenoptera.
OX NCBI_TaxID=9767;
RN [1]
RP SEQUENCE.
RX MEDLINE=76277855; PubMed=962870;
RA Emmens M., Welling G.W., Beintema J.J.;
RT "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
RT ribonuclease."
RL Biochem. J. 157:317-323(1976).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Pancreas.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.

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RL J. Biochem. 106:729-735(1989).
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 DR PIR: JX0085; JX0085.
 DR HSP: P11916; 1B04.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase Pc; 1.
 DR PROSITE: PS00127; RNASE PANCREATIC; 1.
 DR KX Hydroxylase; Nuclease; Endonuclease; 3D-structure;
 KW Pyroliadone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35 BY SIMILARITY.
 FT ACT_SITE 104 104 BY SIMILARITY.
 FT DISULFID 19 72 BY SIMILARITY.
 FT DISULFID 34 82 BY SIMILARITY.
 FT DISULFID 52 97 BY SIMILARITY.
 FT DISULFID 94 111 PROBABLE.
 SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;
 Query Match 60.9%; Score 369; DB 1; Length 111;
 Best Local Similarity 65.5%; Pred. No. 6.4e-33;
 Matches 72; Conservative 9; Mismatches 27; Indels 2; Gaps 2;
 QY 3 NWATFOQKHIIINPPII-CNTIMDNIIYVGGCKRVNTFIISATVKAICTGVI-MNMV 60
 Db 2 NNAKFEKHIRSTSDICNTIMDKAIYVGGCKERTFIISSEDNVKAICSGVSPDRKE 61
 QY 61 LSTTRFQNLTCRTSTITPRPCPYSSRTETNYICVKCENQVPHFAGIGRC 110
 Db 62 LSTTSFKLNTCTRDSTITPRPCPYSPDNKKICVKCKQLPVHFGVIGKC 111
 RESULT 4
 RN30_RANPI STANDARD; PRT; 104 AA.
 ID RN30_RANPI
 AC P22069;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE P-30 protein (EC 3.1.27.-) (Onconase).
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8404;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=91093131; PubMed=1985896;
 RA Ardelit W., Mikulski S.M., Shogen K.;
 RT "Amino acid sequence of an anti-tumor protein from Rana pipiens
 RT oocytes and early embryos. Homology to pancreatic ribonucleases.";
 RL J. Biol. Chem. 266:245-251(1991).
 RN [2]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=93066156; PubMed=1438177;
 RA Mosimann S.C., Johns K.L., Ardelit W., Mikulski S.M., Shogen K.,
 RA James M.N.G.;
 RT "Comparative molecular modeling and crystallization of p-30 protein:
 RT a novel antitumor protein of Rana pipiens oocytes and early
 RT embryos.";
 RL Proteins 14:392-400(1992).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
 RX MEDLINE=94166079; PubMed=8120892;
 RA Mosimann S.C., Ardelit W., James M.N.G.;
 RT "Refined 1.7 A x-ray crystallographic structure of p-30 protein, an
 RT amphibian ribonuclease with anti-tumor activity.";
 RL J. Mol. Biol. 236:1141-1153(1994).

CC -!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity
 CC against several tumor cell lines in vitro, as well as antitumor
 CC in vivo. It exhibits a ribonuclease-like activity against high
 CC molecular weight ribosomal RNA.
 CC -!- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 DR PDB: 1ONC; 31-JAN-94.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase Pc; 1.
 DR PROSITE: PS00127; RNASE PANCREATIC; 1.
 DR KX Hydroxylase; Nuclease; Endonuclease; 3D-structure;
 KW Pyroliadone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 10 10
 FT ACT_SITE 31 31
 FT ACT_SITE 97 97
 FT DISULFID 19 68
 FT DISULFID 30 75
 FT DISULFID 48 90
 FT DISULFID 87 104
 FT HELIX 3 10
 FT STRAND 11 12
 FT HELIX 19 22
 FT STRAND 23 24
 FT TURN 26 30
 FT TURN 26 30
 FT STRAND 33 38
 FT HELIX 41 45
 FT HELIX 46 48
 FT TURN 49 50
 FT TURN 49 50
 FT STRAND 55 58
 FT STRAND 63 70
 FT TURN 74 75
 FT STRAND 77 84
 FT STRAND 86 91
 FT TURN 92 93
 FT STRAND 94 101
 SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;
 Query Match 45.0%; Score 272.5; DB 1; Length 104;
 Best Local Similarity 49.1%; Pred. No. 1.4e-22;
 Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
 QY 3 NWATFOQKHIIINPPII-CNTIMDNIIYVGGCKRVNTFIISATVKAICTGVI-MNMV 60
 Db 2 DMTTFQKHITITRDVDCNIMSTNLF---HCKDNFTIYSRPEPVKAICKGLIASKNV 57
 QY 61 LSTTRFQNLTCRTSTITPRPCPYSSRTETNYICVKCENQVPHFAGIGRC 110
 Db 58 LITSEFYLSDC---NVTSPCKYKLLKSTNKFCVTCENQAPVHFVGVC 104
 RESULT 5
 ANG3_MOUSE STANDARD; PRT; 145 AA.
 ID ANG3_MOUSE
 AC P97802;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)
 DE (BF-5).
 GN ANG3 OR ANGL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=97184476; PubMed=9032278;
 RT Fu X., Kamps M.P.;
 RT "E2a-Pbx1 induces aberrant expression of tissue-specific and

OX	NCBI_TaxID=8400;
RN	[1]_
RP	SEQUENCE.
TX	TISSUE=Liver;
RC	MEDLINE=90130374; PubMed=2613682;
RX	Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
RA	Okazaki T., Ohgi K., Irie M.;
RT	"Primary structure of a ribonuclease from bullfrog (<i>Rana catesbeiana</i>)
RT	liver.";

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OM protein - protein search, using sw model

Run on: May 11, 2004, 14:24:28 ; Search time 10.0452 Seconds
(without alignments)
575.375 Million cell updates/sec

Title: US-09-961-400-26
Perfect score: 606
Sequence: 1 MSNWATFOQKHINTPIICN.....ICVKCNQYPVHFAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	586.5	96.8	133	1 RNPO_RANCA	P11916 rana catesb
2	450	74.3	111	1 LECS_RANCA	P18839 rana japoni
3	369	60.9	111	1 RNPL_RANCA	P14626 rana catesb
4	272.5	45.0	104	1 RN30_RANPI	P22069 rana pipien
5	154.5	25.5	145	1 ANG3_MOUSE	P97802 mus musculu
6	149.5	24.7	145	1 ANG_MOUSE	P64438 mus musculu
7	135.5	22.4	124	1 RNP_BALAC	P00673 balaenopter
8	135.5	22.4	145	1 ANG1_MOUSE	P21570 mus musculu
9	133.5	22.0	167	1 RNBR_BOVIN	P39873 bos taurus
10	132.5	21.9	124	1 RNP_PIG	P00671 sus scrofa
11	128.5	21.2	151	1 RNBR_CAPCA	P79351 capreolus c
12	127.5	21.0	123	1 ANG2_BOVIN	P80929 bos taurus
13	127.5	21.0	141	1 RNBR_GIRCA	Q29542 giraffa cam
14	127.5	21.0	151	1 RNBR_AXIPR	P87350 axis porcin
15	126.5	20.9	119	1 RNP_IGUIG	P80287 iguana igua
16	126.5	20.9	146	1 ANG1_CERAE	O8wn66 cercopithe
17	126.5	20.9	146	1 ANG1_MIOTA	O8wn65 miopithec
18	125	20.6	146	1 ANG1_SALSC	O8wn60 saimiri sci
19	123.5	20.4	143	1 RNBR_SHEEP	Q29543 ovis aries
20	122.5	20.2	124	1 RNP_ANTACR	P00668 antilocapra
21	122	20.1	122	1 RNP_MACRU	P00686 macropus ru
22	120.5	19.9	128	1 RNP_MYOCO	P00676 myocastor c
23	120.5	19.9	147	1 ANG1_PONPY	O8wn67 pongo pygma
24	120.5	19.9	149	1 RNP_MOUSE	P00683 mus musculu
25	120	19.8	146	1 ANG1_AOTIR	O8wn61 aotus trivi
26	119.5	19.7	123	1 ANG1_PIG	P31346 sus scrofa
27	118.5	19.6	128	1 RNBP_CAVPO	P00679 cavia porce
28	118	19.5	146	1 ANG1_SAGOE	O8wn62 saginus oe
29	117.5	19.4	128	1 RNP_HORSE	P00674 equus cabal
30	116.5	19.2	124	1 RNP_CAMDR	P00670 camelus dro
31	116.5	19.2	128	1 RNP_PROGU	P04059 proechinys
32	115.5	19.1	119	1 RN54_BOVIN	P15467 bos taurus
33	115.5	19.1	146	1 ANG1_MACMU	O8wn63 macaca mula

34	114	18.8	148	1 ANGI_BOVIN	P10152 bos taurus
35	113.5	18.7	124	1 RNP_RANTA	P00666 rangifer ta
36	113.5	18.7	125	1 ANGI_RABIT	P31347 oryctolagus
37	113.5	18.7	146	1 ANGI_PAPHA	O8wn64 papio hamad
38	113	18.6	147	1 ANGI_HUMAN	P03950 homo sapien
39	113	18.6	147	1 ANGI_PANTR	O8wn68 pan troglod
40	112.5	18.6	124	1 RNP_CAPCA	P00664 capreolus c
41	112.5	18.6	124	1 RNP_GIRCA	P00662 giraffa cam
42	112.5	18.6	148	1 RN54_MOUSE	O9jjh1 mus musculu
43	111.5	18.4	130	1 RNP_CRILLO	P24717 cricetus
44	111.5	18.4	147	1 RN54_RAT	O55004 rattus norv
45	111.5	18.4	149	1 RNP_ACOCA	Q9wt55 acomys cahi

ALIGNMENTS

RESULT 1

RNPO_RANCA STANDARD; PRT; 133 AA.

AC P11916: Q9PWR7;

DT 01-OCT-1989 (Rel. 12, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DE 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).

DE binding lectin) (SBL-C).

GN RCR.

OS Rana catesbeiana (Bull frog).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoldea; Ranidae; Rana.

OX NCBI_TaxID=8400;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=98165825; PubMed=9497370;

RA Huang H.C., Wang S.C., Ieu Y.J., Lu S.C., Liao Y.D.;

RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.

RT Tissue distribution, cloning, purification, cytotoxicity, and active

RT residues for RNase activity";

RL J. Biol. Chem. 273:6395-6401(1998).

RN [2]

RP SEQUENCE OF 23-133.

RC TISSUE=Egg;

RX MEDLINE=87299649; PubMed=3304421;

RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,

RA Takayanagi G., Hakomori S.;

RA "Amino acid sequence of sialic acid binding lectin from frog (Rana

RT catesbeiana) eggs";

RL Biochemistry 26:2189-2194(1987).

RN [3]

RP CHARACTERIZATION, AND SEQUENCE OF 81-101.

RX MEDLINE=92220613; PubMed=1373237;

RA Liao Y.-D.;

RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana

RT catesbeiana (bullfrog) oocytes.";

RL Nucleic Acids Res. 20:1371-1377(1992).

RN [4]

RP CHARACTERIZATION.

RC TISSUE=Egg;

RX MEDLINE=93192604; PubMed=8448385;

RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,

RA Takayanagi Y., Hakomori S., Titani K.;

RT "Ribonuclease activity of sialic acid-binding lectin from Rana

RT catesbeiana eggs";

RL Glycobiology 3:37-45(1993).

RN [5]

RP STRUCTURE BY NMR OF 23-133.

RX MEDLINE=98437383; PubMed=9761686;

RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;

RT "The solution structure of a cytotoxic ribonuclease from the oocytes

RT of Rana catesbeiana (bullfrog).";

RL J. Mol. Biol. 283:231-244(1998).

CC 1- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine

Search completed: May 11, 2004, 14:39:23
Job time : 38.8281 secs

; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at
; OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
; OTHER INFORMATION: (recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6)
US-09-948-391A-22

Query Match 98.3%; Score 591; DB 10; Length 117;
Best Local Similarity 98.2%; Pred. No. 2.7e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFOOKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
Db 9 NWATFOOKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 68

QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 69 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 13
US-09-961-400-22
; Sequence 22, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-22

Query Match 98.3%; Score 591; DB 10; Length 117;
Best Local Similarity 98.2%; Pred. No. 2.7e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFOOKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
Db 9 NWATFOOKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 68

QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

Db 69 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 14
US-09-948-391A-19
; Sequence 19, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and
; OTHER INFORMATION: Met57Leu substitutions (recombinant RaCOR1
; OTHER INFORMATION: Met22Leu Met57Leu)
US-09-948-391A-19

Query Match 97.3%; Score 585; DB 10; Length 110;
Best Local Similarity 97.2%; Pred. No. 1.2e-58;
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NWATFOOKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
Db 2 NWATFOOKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61

QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 15
US-09-948-391A-11
; Sequence 11, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 104

Qy 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGRCP 110
|||
Db 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGRCP 110

RESULT 9

US-09-948-391A-17
; Sequence 17, Application US/09948391A
; Publication No. US20030027311A1

```

; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-3431100US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
; OTHER INFORMATION: catesbeiana ribonuclease with M
; OTHER INFORMATION: (recombinant Met(-1) RaCOR1)
US-09-948-391A-17

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Query Match	98.3%	Score 591;	DB 10;	Length 111;
Best Local Similarity	99.1%	Pred. No. 2.5e-59;		
Matches 108;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

[illegible][illegible]

RESULT 10

US-09-948-391A-21
; Sequence 21, Application US/09948391A
; Publication No. US20030027311A1

/ GENERAL INFORMATION:
 / APPLICANT: Rybak, Susanna M.
 / APPLICANT: Newton, Dianne L.
 / APPLICANT: The United States of America
 / APPLICANT: as represented by The Secretary of the
 / APPLICANT: Department of Health and Human Services
 / TITLE OF INVENTION: Recombinant Anti-Tumor RNase
 / FILE REFERENCE: 015280-343110US
 / CURRENT APPLICATION NUMBER: US/09/948,391A
 / CURRENT FILING DATE: 2002-05-10
 / PRIOR APPLICATION NUMBER: US 60/079,751
 / PRIOR FILING DATE: 1998-03-27
 / PRIOR APPLICATION NUMBER: WO PCT/US99/06641
 / PRIOR FILING DATE: 1999-03-26
 / PRIOR APPLICATION NUMBER: US 09/622,613
 / PRIOR FILING DATE: 2000-08-17
 / NUMBER OF SEQ ID NOS: 43
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 21

```

; LENGTH: 111
; TYPE: PRT
; ORGANISM: A
; FEATURE:

```

OTHER INFORMATION: Description of Artificial Sequence:Rana
OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1,
OTHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant
OTHER INFORMATION: Met (-1) RACOR1 Met22Leu Met57Leu
US-09-948-391A-21

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Query Match          98.3%; Score 591; DB 10; Length 111;
Best Local Similarity 98.2%; Pred. No. 2.5e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0;
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Q7

2 NWATFQQKHINTPIICNTIMDNNIYVGQCKRVNFISSATVKAICTGVINNVLS 61
||| | ||| : ||| | ||| | ||| : |||

D6

3 NWATFOOQHINTPIICNTIDNNIYVGQCKRVNFISSATVKAICTGVINNVLS 62
||| | ||| : ||| | ||| | ||| : |||

	62	TTRFQNTCTRTSTTPRCPVSSRTETNYICVKCENQYPVHFAGIGRCP	110
QY			
	63	TTRFQNTCTRTSTTPRCPVSSRTETNYICVKCENQYPVHFAGIGRCP	111
pB			

RESULT 11

US-09-961-400-21
; Sequence 21, Application US/09961400
; Publication No. US20030124131A1

; REBUTAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.

Query Match 98.3%; Score 591; DB 10; Length 111;
Best Local Similarity 98.2%; Pred. No. 2.5e-59;
Matches 107; Conservative 2; Mismatches 0; Indels

Qy	2	NWATFQQKHINTPIICNTIMDNNIYVGQCKRVNTHISSATTVKAICTGVINNVLS	61
		: : :	
Db	3	NWATFQQKHINTPIICNTILDNNIYVGQCKRVNTHISSATTVKAICTGVINNVLS	62

Qy	62 TTRFQLNCTRTSTITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db	63 TTRFQLNCTRTSTITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 12

US-09-948-391A-22
; Sequence 22, Application US/09948391A
; Publication No. US20030027311A1

; GENERAL INFORMATION:
 ; APPLICANT: Rybak, Susanna M.
 ; APPLICANT: Newton, Dianne L.
 ; APPLICANT: The United States of America
 ; APPLICANT: as represented by The Secretary of the
 ; APPLICANT: Department of Health and Human Services

```

; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
; OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match          99.3%; Score 597; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.2e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2  NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
Db  2  NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61

QY  62  TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110
Db  62  TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110

RESULT 6
US-09-961-400-15
; Sequence 15, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-15

Query Match          99.3%; Score 597; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.2e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2  NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
Db  2  NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61

QY  62  TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110
Db  62  TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110

```

```

; Sequence 17, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-17

Query Match          99.3%; Score 597; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 5.3e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2  NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
Db  3  NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 62

QY  62  TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110
Db  63  TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 111

RESULT 8
US-09-961-400-19
; Sequence 19, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-19

Query Match          98.3%; Score 591; DB 10; Length 110;
Best Local Similarity 98.2%; Pred. No. 2.5e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  2  NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
Db  2  NWATFOQKHINTPIICNTILNDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61

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RESULT 7
US-09-961-400-17

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Db 1 SNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVNNVL 60
Qy 61 STTRFQTLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 61 STTRFQTLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110

RESULT 2
US-09-961-400-24
; Sequence 24, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-24

Query Match 100.0%; Score 601; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.8e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVNNVL 60
Db 1 SNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVNNVL 60
Qy 61 STTRFQTLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 61 STTRFQTLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110

RESULT 3
US-09-948-391A-26
; Sequence 26, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: NEWTON, DIANNE L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: and Gln2Ser substitution (Met(-1) RacOR1 Q1S)
US-09-948-391A-26

Query Match 100.0%; Score 601; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.8e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVNNVL 60
Db 1 SNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVNNVL 61
Qy 61 STTRFQTLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 62 STTRFQTLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 4
US-09-961-400-26
; Sequence 26, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-26

Query Match 100.0%; Score 601; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.8e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 SNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVNNVL 61
Qy 61 STTRFQTLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 62 STTRFQTLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 5
US-09-948-391A-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: NEWTON, DIANNE L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 14:34:38 ; Search time 37.8281 Seconds
(without alignments)
807.135 Million cell updates/sec

Title: US-09-961-400-24
Perfect score: 601
Sequence: 1 SNWATFQKHINTPICNT.....ICVKCNQYVPHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277565755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	601	100.0	110	10	US-09-948-391A-24
2	601	100.0	110	10	US-09-961-400-24
3	601	100.0	111	10	US-09-948-391A-26
4	601	100.0	111	10	US-09-961-400-26
5	597	99.3	110	10	US-09-948-391A-15
6	597	99.3	110	10	US-09-961-400-15
7	597	99.3	111	10	US-09-961-400-17
8	591	98.3	110	10	US-09-961-400-19
9	591	98.3	111	10	US-09-948-391A-17
10	591	98.3	111	10	US-09-948-391A-21
11	591	98.3	111	10	US-09-961-400-21
12	591	98.3	117	10	US-09-948-391A-22
13	591	98.3	117	10	US-09-961-400-22
14	585	97.3	110	10	US-09-948-391A-19
15	280.5	46.7	104	10	US-09-948-391A-11

16	280.5	46.7	104	10	US-09-961-400-11	Sequence 11, Appl
17	280.5	46.7	105	10	US-09-948-391A-13	Sequence 13, Appl
18	280.5	46.7	105	10	US-09-961-400-13	Sequence 13, Appl
19	276.5	46.0	104	10	US-09-961-400-2	Sequence 2, Appl
20	276.5	46.0	105	10	US-09-948-391A-6	Sequence 6, Appl
21	276.5	46.0	105	10	US-09-961-400-6	Sequence 6, Appl
22	276.5	46.0	127	10	US-09-948-391A-28	Sequence 28, Appl
23	276.5	46.0	127	10	US-09-961-400-28	Sequence 28, Appl
24	275.5	45.8	104	10	US-09-948-391A-2	Sequence 2, Appl
25	273.5	45.5	111	10	US-09-961-400-9	Sequence 9, Appl
26	272.5	45.3	104	9	US-09-966-119-1	Sequence 1, Appl
27	272.5	45.3	104	10	US-09-918-887-1	Sequence 1, Appl
28	272.5	45.3	105	14	US-10-153-882-2	Sequence 2, Appl
29	270.5	45.0	104	10	US-09-948-391A-4	Sequence 4, Appl
30	270.5	45.0	104	10	US-09-961-400-4	Sequence 4, Appl
31	270.5	45.0	105	10	US-09-961-400-8	Sequence 8, Appl
32	264.5	44.0	104	12	US-10-461-713-53	Sequence 53, Appl
33	261.5	43.5	105	10	US-09-948-391A-8	Sequence 8, Appl
34	261.5	43.5	111	10	US-09-948-391A-9	Sequence 9, Appl
35	206	34.3	83	9	US-09-986-119-3	Sequence 3, Appl
36	206	34.3	83	10	US-09-918-887-3	Sequence 3, Appl
37	158	26.3	169	13	US-10-016-447-2	Sequence 2, Appl
38	135.5	22.5	124	12	US-10-037-417-103	Sequence 103, App
39	126.5	21.0	119	12	US-10-016-248-89	Sequence 89, Appl
40	126.5	21.0	119	15	US-10-074-978A-139	Sequence 139, Appl
41	121	20.1	99	15	US-10-074-978A-141	Sequence 141, App
42	117.5	19.6	124	12	US-10-461-713-52	Sequence 52, Appl
43	117	19.5	147	9	US-09-731-872-254	Sequence 254, App
44	117	19.5	147	10	US-09-876-997-254	Sequence 254, App
45	114.5	19.1	124	9	US-09-981-286A-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1

US-09-948-391A-24
; Sequence 24, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Gln1ser substitution
; OTHER INFORMATION: (recombinant RACOR1 Q1S)
US-09-948-391A-24

Query Match 100.0%; Score 601; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.8e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 SNWATFQKHINTPICNTIMDNNTIYVGQCKRVNTFISSATTVKALCTGVNNVL 60
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DT	01-JUN-2003	(TtEMBLrel. 24, Created)			
DT	01-JUN-2003	(TtEMBLrel. 24, Last sequence update)			
DT	01-OCT-2003	(TtEMBLrel. 25, Last annotation update)			
DE	Angiogenin.				
OS	Pygathrix roxellana (golden snub-nosed monkey).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;				
OC	Pygathrix.				
OX	NCBI_TaxID=61622;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=22597544; PubMed=12711394;				
RA	Zhang J., Zhang Y.-P.;				
RT	"Pseudogenization of the tumor-growth promoter angiogenin in a leaf-				
RL	eating monkey.";				
RL	Gene 308:95-101(2003).				
DR	EMBL; AY221130; AA041337.1; -.				
DR	GO; GO:0003676; F:nuclieic acid binding; IEA.				
DR	GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.				
DR	InterPro; IPR001427; RNaseA.				
DR	Pfam; PF00074; rnasea; 1.				
DR	PRINTS; PR00794; RIBONUCLEASE.				
DR	ProDom; PD000535; RNaseA; 1.				
DR	SMART; SMC0092; RNase_Pc; 1.				
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.				
SQ	SEQUENCE 146 AA; 16438 MW; 8CF170A4BD12BA67 CRC64;				
Query Match	22.4%;	Score 129.5;	DB 6;	Length 146;	
Best Local Similarity	34.2%;	Pred. No. 4.1e-07;			
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DB	31	RDPLT---KHVDATPQGRNDRYCESMWRGRTSPCKDNTFTHGNSRHKACGDGNGN			
QY	52	IASKNY-LITTFEYLSDCNV---TSR-PCKYKLKSTNTFCVTCENQAPVH	97		
DB	88	PYGENLRISKSPFQVITCNLGGSSRPFCYRATAGFRIVVACENDLPEVH	138		
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AC	Q861Y2;				
DT	01-JUN-2003	(TtEMBLrel. 24, Created)			
DT	01-JUN-2003	(TtEMBLrel. 24, Last sequence update)			
DT	01-OCT-2003	(TtEMBLrel. 25, Last annotation update)			
DE	Angiogenin.				
OS	Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;				
OC	Pygathrix.				
OX	NCBI_TaxID=61621;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=22597544; PubMed=12711394;				
RA	Zhang J., Zhang Y.-P.;				
RT	"Pseudogenization of the tumor-growth promoter angiogenin in a leaf-				
RL	eating monkey.";				
RL	Gene 308:95-101(2003).				
DR	EMBL; AY221131; AA041338.1; -.				
DR	GO; GO:0003676; F:nuclieic acid binding; IEA.				
DR	GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.				
DR	InterPro; IPR001427; RNaseA.				
DR	Pfam; PF00074; rnasea; 1.				
DR	PRINTS; PR00794; RIBONUCLEASE.				
DR	ProDom; PD000535; RNaseA; 1.				
DR	SMART; SMC0092; RNase_Pc; 1.				
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.				
SQ	SEQUENCE 146 AA; 16438 MW; 8CF170A4BD12BA67 CRC64;				

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DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE RNase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
CX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351208; AAK30254.1; -.
DR HSSP; P11916; 18C4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 1 22 POTENTIAL.
Query Match 48.4%; Score 280; DB 13; Length 132;
Best Local Similarity 48.6%; Pred. No. 1.3e-24;
Matches 54; Conservative 14; Mismatches 35; Indels 8; Gaps 3;
Qy 1 QDWLTFQKKHLNTRDVCNIMTNLF---HCKDKNTFYSRPEPVKAICKGLIAASKN 56
Db 23 QDWLTFQKKHLNTRDVCNIMTNLF---HCKDKNTFYSRPEPVKAICKGLIAASKN 56
Qy 57 VLTSEFYLSDCN---VTSRCPCKYKLKSTNTFCVTCENQAPVHFVGVGHC 104
Db 23 VLTSEFYLSDCN---VTSRCPCKYKLKSTNTFCVTCENQAPVHFVGVGHC 104
Qy 82 VLSTTRFQKXKTRFTITSRCPYSSYTKETNKICVKCENEPVHFVGVGHC 132
Db 82 VLSTTRFQKXKTRFTITSRCPYSSYTKETNKICVKCENEPVHFVGVGHC 132
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AC Q9DF78 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE RC-RNaseL1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
CX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288642; AAG30414.2; -.
DR HSSP; P11916; 18C4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.

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Db 82 VLSTTRPQLNCTRTSITPRPCPYSSRTNNYICVKCNQYVHFAGIGRC 132

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AC Q98SL9

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE RNase A-type ribonuclease rc212 precursor.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI_TaxID=8400;

RN [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=21539506; PubMed=11683320;

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

RT "Rapid diversification of RNase A superfamily ribonuclease from the

RT bullfrog, Rana catesbeiana.";

RL J. Mol. Evol. 53:31-38 (2001).

RN EMBL; AF351210; AAK30256.1; -. HSP; P11916; 1BC4.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; rnaseA; 1.

DR ProDom; PD000535; RNaseA; 1.

DR SMART; SM00092; RNase_Pc; 1.

DR PROSITE; PS00127; RNASE_PANCREATIC; 1.

DR SIGNAL.

FT CHAIN 1 22 POTENTIAL.

FT SIGNAL 23 132 RC-RNase7.

SQ SEQUENCE 133 AA; 14615 MW; C8785B26B26E54E CRC64;

Query Match 49.5%; Score 286; DB 13; Length 133;

Best Local Similarity 47.7%; Pred. No. 2.6e-25;

Matches 53; Conservative 17; Mismatches 33; Indels 8; Gaps 3;

QY 1 QDWLTFOKKHLNTRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

Db 23 QNWATFQKHINTSSINCNTIMDNNIYVGGQCKKNTFIASSATTVKIGCSG-VTDKK 81

QY 57 VLTTSFYLSDCN--VTSRCKYKLKSTNTFCVTCENQAPVHFVGVGHC 104

Db 82 VLSSTKFQDICTRIFITPRPCPYSSRTETNYICVKCNQYVHFAGIGQC 132

RESULT 9

Q98SM2 PRELIMINARY; PRT; 132 AA.

AC Q98SM2

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI_TaxID=8400;

RN [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=21539506; PubMed=11683320;

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

RT "Rapid diversification of RNase A superfamily ribonuclease from the

RT bullfrog, Rana catesbeiana.";

RL J. Mol. Evol. 53:31-38 (2001).

RN EMBL; AF351211; AAK30257.1; -. HSP; P11916; 1BC4.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; rnaseA; 1.

DR ProDom; PD000535; RNaseA; 1.

DR SMART; SM00092; RNase_Pc; 1.

DR PROSITE; PS00127; RNASE_PANCREATIC; 1.

DR SIGNAL.

FT CHAIN 1 22 POTENTIAL.

FT SIGNAL 23 132 RC-RNase7.

SQ SEQUENCE 133 AA; 14615 MW; C8785B26B26E54E CRC64;

Query Match 49.5%; Score 286; DB 13; Length 133;

Best Local Similarity 47.7%; Pred. No. 2.6e-25;

Matches 53; Conservative 17; Mismatches 33; Indels 8; Gaps 3;

QY 1 QDWLTFOKKHLNTRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

Db 23 QNWATFQKHINTSSINCNTIMDNNIYVGGQCKKNTFIASSATTVKIGCSG-VTDKK 81

QY 57 VLTTSFYLSDCN--VTSRCKYKLKSTNTFCVTCENQAPVHFVGVGHC 104

Db 82 VLSSTKFQDICTRIFITPRPCPYSSRTETNYICVKCNQYVHFAGIGQC 132

RESULT 9

Q98SM2 PRELIMINARY; PRT; 132 AA.

AC Q98SM2

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI_TaxID=8400;

RN [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=21539506; PubMed=11683320;

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

RT "Rapid diversification of RNase A superfamily ribonuclease from the

RT bullfrog, Rana catesbeiana.";

RL J. Mol. Evol. 53:31-38 (2001).

RN EMBL; AF351211; AAK30257.1; -. HSP; P11916; 1BC4.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; rnaseA; 1.

DR ProDom; PD000535; RNaseA; 1.

DR SMART; SM00092; RNase_Pc; 1.

DR PROSITE; PS00127; RNASE_PANCREATIC; 1.

DR SIGNAL.

FT CHAIN 1 22 POTENTIAL.

FT SIGNAL 23 132 RC-RNase7.

SQ SEQUENCE 133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;

Query Match 48.8%; Score 282; DB 13; Length 133;

Best Local Similarity 46.8%; Pred. No. 7.7e-25;

Matches 52; Conservative 18; Mismatches 33; Indels 8; Gaps 3;

QY 1 QDWLTFOKKHLNTRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

Db 23 QNWATFQKHINTSSINCNTIMDNNIYVGGQCKKNTFIASSATTVKIGCSG-VTDKK 81

QY 57 VLTTSFYLSDCN--VTSRCKYKLKSTNTFCVTCENQAPVHFVGVGHC 104

Db 82 VLSSTKFQDICTRIFITPRPCPYSSRTETNYICVKCNQYVHFAGIGQC 132

Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.


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Db      24 QDWLTFQKKHLTNTDRVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 83
QY      61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
Db      84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 2
Q8UVX5 ID Q8UVX5 PRELIMINARY; PRT; 127 AA.
AC Q8UVX5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Onconase precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT "Rana pipiens onconase genomic DNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -.
DR PIR; A39035; A39035.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase P; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;

Query Match
Best Local Similarity 96.2%; Score 556; DB 13; Length 127;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 QDWLTFQKKHLTNTDRVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
Db      24 QDWLTFQKKHLTNTDRVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 83
QY      61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
Db      84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 3
Q9DFY6 ID Q9DFY6 PRELIMINARY; PRT; 129 AA.
AC Q9DFY6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]

Query Match
Best Local Similarity 96.2%; Score 556; DB 13; Length 127;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 QDWLTFQKKHLTNTDRVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
Db      24 QDWLTFQKKHLTNTDRVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 83
QY      61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
Db      84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 4
Q9DFY8 ID Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]

Query Match
Best Local Similarity 96.8%; Score 386; DB 13; Length 128;
Matches 70; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY      1 QDWLTFQKKHLTNTDRVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60

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RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242555; AAG31441.2; -.
DR PDB; 1KVZ; 28-JUL-02.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
FT CHAIN 1 23 POTENTIAL.
FT CHAIN 24 129 RC-RNASE4 RIBONUCLEASE.
SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match
Best Local Similarity 70.0%; Score 404.5; DB 13; Length 129;
Matches 71; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

QY      1 QDWLTFQKKHLTNTDRVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
Db      24 QDWLTFQKKHLTNTDRVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 83
QY      61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
Db      84 SEFYLAECNVKPRCKYKLLKSSNEICIRCEHELPHVHFAGVGIC 128

RESULT 4
Q9DFY8 ID Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]

Query Match
Best Local Similarity 66.8%; Score 386; DB 13; Length 128;
Matches 70; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY      1 QDWLTFQKKHLTNTDRVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.5753 Seconds
(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-2
Perfect score: 578
Sequence: 1 QDLWTFQKKHLNTRDVCN.....TFCVTCENQAPVHFVGVGHC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPTREMBL 25:*

2: sp_archaea:*

3: sp_bacteria:*

4: sp_fungi:*

5: sp_human:*

6: sp_invertebrate:*

7: sp_mammal:*

8: sp_mhc:*

9: sp_organelle:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	578	100.0	127	13 Q918V8	Q918V8 rana pipien
2	556	96.2	127	13 Q8UVX5	Q8UVX5 rana pipien
3	404.5	70.0	129	13 Q9DFY6	Q9dfy6 rana catesb
4	386	66.8	128	13 Q9DFY8	Q9dfy8 rana catesb
5	311	53.8	128	13 Q9DFY7	Q9dfy7 rana catesb
6	309	53.5	128	13 Q9DFY5	Q9dfy5 rana catesb
7	298	51.6	133	13 Q98SM0	Q98sm0 rana catesb
8	286	49.5	133	13 Q98SL9	Q98sl9 rana catesb
9	285	49.3	132	13 Q98SM2	Q98sm2 rana catesb
10	282	48.4	133	13 Q98SL8	Q98sl8 rana catesb
11	280	48.4	132	13 Q98SM1	Q98sm1 rana catesb
12	275.5	47.7	132	13 Q9DF78	Q9df78 rana catesb
13	157.5	27.2	169	13 Q9W738	Q9w738 xenopus lae
14	129.5	22.4	146	6 Q861Y3	Q861y3 pygathrix r
15	129.5	22.4	146	6 Q861Y2	Q861y2 pygathrix b
16	129.5	22.4	146	6 Q861Y1	Q861y1 pygathrix a

17	129	22.3	152	11 Q9JK15	Q9jki5 mus saxicol
18	127	22.0	157	11 Q9JK19	Q9jki9 meriones un
19	126.5	21.9	153	11 Q9JK17	Q9jki7 mus saxicol
20	126	21.8	157	11 Q9JK03	Q9jki3 meriones un
21	125.5	21.7	146	6 Q861Y4	Q861y4 trachypithe
22	125	21.6	157	11 Q9JKJ4	Q9jkj4 meriones un
23	123	21.3	154	11 Q9JK18	Q9jki8 mus saxicol
24	122	21.1	157	11 Q9JKJ1	Q9jkj1 meriones un
25	121	20.9	147	6 Q7YRJ6	Q7yrj6 balaena mys
26	121	20.9	157	11 Q9JKJ2	Q9jkj2 meriones un
27	120.5	20.8	155	11 Q9JKH9	Q9jkh9 mus pahari
28	119.5	20.7	155	11 Q9JKI3	Q9jki3 mus saxicol
29	118	20.4	147	6 Q7YRJ5	Q7yrj5 tursiops tr
30	116.5	20.2	155	11 Q9JKI6	Q9jki6 mus saxicol
31	115.5	20.0	132	6 Q9TV25	Q9tv25 eulemur ful
32	115.5	20.0	155	11 Q9JKI2	Q9jki2 mus saxicol
33	115.5	20.0	155	11 Q9JKI4	Q9jki4 mus saxicol
34	115	19.9	146	6 Q861Y5	Q861y5 colobus que
35	114.5	19.8	170	6 Q9BEC1	Q9bec1 tragulus ja
36	113.5	19.6	119	6 Q9TSQ6	Q9tsq6 cercopithec
37	113.5	19.6	119	6 Q9TV32	Q9tv32 gorilla gor
38	113.5	19.6	132	6 Q9TV24	Q9tv24 galago moho
39	113.5	19.6	147	6 Q8HZQ0	Q8hzq0 pan troglod
40	113.5	19.6	155	11 Q9R134	Q9r134 rattus norv
41	113	19.6	156	11 Q9JKG6	Q9jkg6 mus caroli
42	113	19.6	156	11 Q9JKH7	Q9jkh7 mus caroli
43	112.5	19.5	119	6 Q9TV30	Q9tv30 saguinus oe
44	112.5	19.5	155	11 Q9R125	Q9r125 mus musculu
45	112.5	19.5	155	11 Q9JKH8	Q9jkh8 mus pahari

ALIGNMENTS

RESULT 1

Q918V8
ID Q918V8 PRELIMINARY; PRT; 127 AA.
AC Q918V8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Onconase variant rap1R1 precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure.";
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165113; AAF76935.1; -
DR PIR; A39035; A39035.
DR HSSP; P22069; 10NC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00032; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 100.0%; Score 578; DB 13; Length 127;

Best Local Similarity 100.0%; Pred.No. 3.5e-59;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDLWTFQKKHLNTRDVCNIMSTNLFCHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60

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;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with Met at position 1 and GlnSer
; OTHER INFORMATION: substitution (recombinant Met(-1) RaPLR1 Q1S)
US-09-948-391A-13

Query Match          47.1%; Score 285.5; DB 10; Length 105;
Best Local Similarity 50.0%; Pred. No. 1,2e-34;
Matches      56; Conservative 15; Mismatches 32; Indels   9; Gaps    4;

QY      1 MSNWATFOOKHIINT-PIICNTIMDNNIYIVGCKKRVNTPFISSATTVAICTGVI-NM 58
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       1 MSDWLTFOKKHLTNTRDVCNNIMSTNLP---HCKDKNTFYISRPFPVKAICKGIASK 56

QY      59 NVLSTTRFQNLCTRTYSITFRPCPYCSRSRTETNYICVKCNQYPVHFAGIGRC 110
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       57 NVLTTSEFYLSDC---NVTSRPCYKYLKKSNTNFVTCENQAQPVHFVGVGHC 105
```

```
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR FILING DATE: 09/622,613
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-22

Query Match          98.3%; Score 596; DB 10; Length 117;
Best Local Similarity 97.3%; Pred. No. 7e-60;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNWATFOQKHIIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
DB 7 MONWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 66

QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 67 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 13
US-09-961-400-19
; Sequence 19, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR FILING DATE: 09/622,613
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-19

Query Match          97.5%; Score 591; DB 10; Length 110;
Best Local Similarity 98.2%; Pred. No. 2.4e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 NWATFOQKHIIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 62
DB 2 NWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLVLS 61

QY 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
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DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 14
US-09-948-391A-19
; Sequence 19, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: NEWTON, DIANNE L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and
; OTHER INFORMATION: Met57Leu substitutions (recombinant RaCOR1
; OTHER INFORMATION: Met22Leu Met57Leu)
US-09-948-391A-19

Query Match          96.5%; Score 585; DB 10; Length 110;
Best Local Similarity 97.2%; Pred. No. 1.2e-58;
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 NWATFOQKHIIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 62
DB 2 NWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLVLS 61

QY 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 15
US-09-948-391A-13
; Sequence 13, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: NEWTON, DIANNE L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 105
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QY 1 MSNWATFQOKHIINTPIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVINNV 60
Db 1 MQNWATFQOKHIINTPIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVINNV 60
QY 61 LSTTRFQLTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQLTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 9
US-09-948-391A-21
; Sequence 21, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1,
; OTHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant
; OTHER INFORMATION: Met(-1) RaCOR1 Met22Leu Met57Leu)
US-09-948-391A-21

Query Match 98.3%; Score 596; DB 10; Length 111;
Best Local Similarity 97.3%; Pred. No. 6.6e-60;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNWATFQOKHIINTPIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVINNV 60
Db 1 MQNWATFQOKHIINTPIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVINNV 60
QY 61 LSTTRFQLTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQLTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 10
US-09-961-400-21
; Sequence 21, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
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; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-21

Query Match 98.3%; Score 596; DB 10; Length 111;
Best Local Similarity 97.3%; Pred. No. 6.6e-60;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNWATFQOKHIINTPIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVINNV 60
Db 1 MQNWATFQOKHIINTPIICNTILDNIIYVGGCKRVNTFISSATTVKAICTGVINLV 60
QY 61 LSTTRFQLTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQLTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 11
US-09-948-391A-22
; Sequence 22, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at
; OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
; OTHER INFORMATION: (recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6)
US-09-948-391A-22

Query Match 98.3%; Score 596; DB 10; Length 117;
Best Local Similarity 97.3%; Pred. No. 7e-60;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNWATFQOKHIINTPIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVINNV 60
Db 7 MQNWATFQOKHIINTPIICNTILDNIIYVGGCKRVNTFISSATTVKAICTGVINLV 66
QY 61 LSTTRFQLTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 67 LSTTRFQLTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 12
US-09-961-400-22
; Sequence 22, Application US/09961400
; Publication No. US20030124131A1
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/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: 60/079,751
/ PRIOR FILING DATE: 1998-03-26
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 24
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Rana catesbeiana
US-09-961-400-24

Query Match
Best Local Similarity 99.2%; Score 601; DB 10; Length 110;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SNWATFQOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 61
DB 1 SNWATFQOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 60
QY 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 6
US-09-948-391A-15
/ Sequence 15, Application US/09948391A
/ Publication No. US20030027311A1
/ GENERAL INFORMATION:
/ APPLICANT: Rybak, Susanna M.
/ APPLICANT: Newton, Dianne L.
/ APPLICANT: The United States of America
/ APPLICANT: as represented by The Secretary of the
/ APPLICANT: Department of Health and Human Services
/ TITLE OF INVENTION: Recombinant Anti-Tumor RNase
/ FILE REFERENCE: 015280-343110US
/ CURRENT APPLICATION NUMBER: US/09/948,391A
/ CURRENT FILING DATE: 2002-05-10
/ PRIOR APPLICATION NUMBER: US 60/079,751
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: WO PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: US 09/622,613
/ PRIOR FILING DATE: 2000-08-17
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 15
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Rana
/ OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
/ OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match
Best Local Similarity 98.5%; Score 597; DB 10; Length 110;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NWATFQOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 62
DB 2 NWATFQOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 61
QY 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 7
US-09-961-400-15
/ Sequence 15, Application US/09948391A
/ Publication No. US20030027311A1
/ GENERAL INFORMATION:
/ APPLICANT: Rybak, Susanna M.
/ APPLICANT: Newton, Dianne L.
/ APPLICANT: The United States of America
/ APPLICANT: as represented by The Secretary of the
/ APPLICANT: Department of Health and Human Services
/ TITLE OF INVENTION: Recombinant Anti-Tumor RNase
/ FILE REFERENCE: 015280-343110US
/ CURRENT APPLICATION NUMBER: US/09/948,391A
/ CURRENT FILING DATE: 2002-05-10
/ PRIOR APPLICATION NUMBER: US 60/079,751
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: WO PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: US 09/622,613
/ PRIOR FILING DATE: 2000-08-17
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 15
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Rana
/ OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
/ OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match
Best Local Similarity 100.0%; Pred. No. 5e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NWATFQOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 62
DB 2 NWATFQOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 61
QY 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 7
US-09-961-400-15
/ Sequence 15, Application US/09948391A
/ Publication No. US20030027311A1
/ GENERAL INFORMATION:
/ APPLICANT: Rybak, Susanna M.
/ APPLICANT: Newton, Dianne L.
/ APPLICANT: The United States of America
/ APPLICANT: as represented by The Secretary of the
/ APPLICANT: Department of Health and Human Services
/ TITLE OF INVENTION: Recombinant Anti-Tumor RNase
/ FILE REFERENCE: 015280-343110US
/ CURRENT APPLICATION NUMBER: US/09/948,391A
/ CURRENT FILING DATE: 2002-05-10
/ PRIOR APPLICATION NUMBER: US 60/079,751
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: WO PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: US 09/622,613
/ PRIOR FILING DATE: 2000-08-17
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 15
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Rana
/ OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
/ OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match
Best Local Similarity 98.5%; Score 597; DB 10; Length 110;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NWATFQOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 62
DB 2 NWATFQOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 61
QY 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 7
US-09-961-400-15
/ Sequence 15, Application US/09948391A
/ Publication No. US20030027311A1
/ GENERAL INFORMATION:
/ APPLICANT: Rybak, Susanna M.
/ APPLICANT: Newton, Dianne L.
/ APPLICANT: The United States of America
/ APPLICANT: as represented by The Secretary of the
/ APPLICANT: Department of Health and Human Services
/ TITLE OF INVENTION: Recombinant Anti-Tumor RNase
/ FILE REFERENCE: 015280-343110US
/ CURRENT APPLICATION NUMBER: US/09/948,391A
/ CURRENT FILING DATE: 2002-05-10
/ PRIOR APPLICATION NUMBER: US 60/079,751
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: WO PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: US 09/622,613
/ PRIOR FILING DATE: 2000-08-17
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 15
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Rana
/ OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
/ OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match
Best Local Similarity 98.3%; Score 596; DB 10; Length 111;
Matches 109; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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/ Sequence 15, Application US/09961400
/ Publication No. US20030124131A1
/ GENERAL INFORMATION:
/ APPLICANT: RYBAK, SUSANNA M.
/ APPLICANT: GOLDENBERG, DAVID M.
/ APPLICANT: NEWTON, DIANNE L.
/ TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
/ TITLE OF INVENTION: CELLS
/ FILE REFERENCE: 018733/1059
/ CURRENT APPLICATION NUMBER: US/09/961,400
/ CURRENT FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: 09/622,613
/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: 60/079,751
/ PRIOR FILING DATE: 1998-03-26
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 15
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Rana catesbeiana
US-09-961-400-15

Query Match
Best Local Similarity 100.0%; Pred. No. 5e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NWATFQOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 62
DB 2 NWATFQOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 61
QY 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 8
US-09-948-391A-17
/ Sequence 17, Application US/09948391A
/ Publication No. US20030027311A1
/ GENERAL INFORMATION:
/ APPLICANT: Rybak, Susanna M.
/ APPLICANT: Newton, Dianne L.
/ APPLICANT: The United States of America
/ APPLICANT: as represented by The Secretary of the
/ APPLICANT: Department of Health and Human Services
/ TITLE OF INVENTION: Recombinant Anti-Tumor RNase
/ FILE REFERENCE: 015280-343110US
/ CURRENT APPLICATION NUMBER: US/09/948,391A
/ CURRENT FILING DATE: 2002-05-10
/ PRIOR APPLICATION NUMBER: US 60/079,751
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: WO PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: US 09/622,613
/ PRIOR FILING DATE: 2000-08-17
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 17
/ LENGTH: 111
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Rana
/ OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
/ OTHER INFORMATION: (recombinant Met(-1) RaCOR1)
US-09-948-391A-17

Query Match
Best Local Similarity 98.2%; Score 596; DB 10; Length 111;
Matches 109; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 1 MSNWATFQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKACTGVINNV 60
Qy 61 LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 2

US-09-961-400-26
; Sequence 26, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-26

Query Match 100.0%; Score 606; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.8e-61;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSNWATFQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKACTGVINNV 60
Db 1 MSNWATFQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKACTGVINNV 60
Qy 61 LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 3

US-09-961-400-17
; Sequence 17, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-17

Query Match 99.3%; Score 602; DB 10; Length 111;
Best Local Similarity 99.1%; Pred. No. 1.4e-60;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSNWATFQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKACTGVINNV 60
Db 1 MSNWATFQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKACTGVINNV 60
Qy 61 LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 4

US-09-948-391A-24
; Sequence 24, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with GluHiser substitution
; OTHER INFORMATION: (recombinant RaCOR1 Q1S)
US-09-948-391A-24

Query Match 99.2%; Score 601; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.8e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SNWATFQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKACTGVINNV 61
Db 1 SNWATFQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKACTGVINNV 60
Qy 62 STTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 STTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 5

US-09-961-400-24
; Sequence 24, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613

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OM protein - protein search, using sw model

Run on: May 11, 2004, 14:34:38 ; Search time 38.1719 Seconds
(without alignments)
807.135 Million cell updates/sec

Title: US-09-961-400-26

Perfect score: 606

Sequence: 1 MSNWATFQKHINTPIICN.....ICVKCNQYVHFAGIGRCP 111

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Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	606	100.0	111	10	US-09-948-391A-26
2	606	100.0	111	10	US-09-961-400-26
3	602	99.3	111	10	US-09-961-400-17
4	601	99.2	110	10	US-09-948-391A-24
5	601	99.2	110	10	US-09-961-400-24
6	597	98.5	110	10	US-09-948-391A-15
7	597	98.5	110	10	US-09-961-400-15
8	596	98.3	111	10	US-09-948-391A-17
9	596	98.3	111	10	US-09-948-391A-21
10	596	98.3	111	10	US-09-961-400-21
11	596	98.3	117	10	US-09-948-391A-22
12	596	98.3	117	10	US-09-961-400-22
13	591	97.5	110	10	US-09-961-400-19
14	585	96.5	110	10	US-09-948-391A-19
15	285.5	47.1	105	10	US-09-948-391A-13

16	285.5	47.1	105	10	US-09-961-400-13	Sequence 13, Appl
17	281.5	46.5	105	10	US-09-948-391A-6	Sequence 6, Appli
18	281.5	46.5	105	10	US-09-961-400-6	Sequence 6, Appli
19	280.5	46.3	104	10	US-09-948-391A-11	Sequence 11, Appl
20	280.5	46.3	104	10	US-09-961-400-11	Sequence 11, Appl
21	278.5	46.0	111	10	US-09-961-400-9	Sequence 9, Appli
22	277.5	45.8	105	14	US-10-153-882-2	Sequence 2, Appli
23	276.5	45.6	104	10	US-09-961-400-2	Sequence 2, Appli
24	276.5	45.6	127	10	US-09-948-391A-28	Sequence 28, Appl
25	276.5	45.6	127	10	US-09-961-400-28	Sequence 28, Appl
26	275.5	45.5	104	10	US-09-948-391A-2	Sequence 2, Appli
27	275.5	45.5	105	10	US-09-961-400-8	Sequence 8, Appli
28	272.5	45.0	104	9	US-09-986-119-1	Sequence 1, Appli
29	272.5	45.0	104	10	US-09-918-887-1	Sequence 1, Appli
30	270.5	44.6	104	10	US-09-948-391A-4	Sequence 4, Appli
31	270.5	44.6	104	10	US-09-961-400-4	Sequence 4, Appli
32	266.5	44.0	105	10	US-09-948-391A-8	Sequence 8, Appli
33	266.5	44.0	111	10	US-09-948-391A-9	Sequence 9, Appli
34	264.5	43.6	104	12	US-10-461-713-53	Sequence 53, Appl
35	206	34.0	83	9	US-09-986-119-3	Sequence 3, Appli
36	206	34.0	83	10	US-09-918-887-3	Sequence 3, Appli
37	158	26.1	169	13	US-10-016-447-2	Sequence 2, Appli
38	135.5	22.4	124	12	US-10-037-417-103	Sequence 103, App
39	126.5	20.9	119	12	US-10-016-248-89	Sequence 89, Appl
40	126.5	20.9	119	15	US-10-074-978A-139	Sequence 139, App
41	121	20.0	99	15	US-10-074-978A-141	Sequence 141, App
42	117.5	19.4	124	12	US-10-461-713-52	Sequence 52, Appl
43	117	19.3	147	9	US-09-731-872-254	Sequence 254, App
44	117	19.3	147	10	US-09-876-997-254	Sequence 254, App
45	114.5	18.9	124	9	US-09-981-286A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-948-391A-26
; Sequence 26, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-3431100S
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: and Gln2Ser substitution (Met(-1) RacOR1 Q1S)
US-09-948-391A-26

Query Match 100.0%; Score 606; DB 10; Length 111;
Best Local Similarity 100.0%; Pred No. 4.8e-61;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSNWATFQKHINTPIICNNTMDNIIYVGCKRVNTFISSATTVKATGVINMV 60
|||||

Q9BEC1	PRELIMINARY;	PRT;	170 AA.
ID	Q9BEC1		
AC	Q9BEC1;		
DT	01-JUN-2001 (TReMBLrel. 17, Created)		
DT	01-JUN-2001 (TReMBLrel. 17, Last sequence update)		
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)		
DE	Brain-type ribonuclease ribonuclease precursor (Fragment).		
DE	RNAse B.		
GN	Tringulus javanicus (Lesser Malay chevrotain).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;		
OC	Tragulidae; Tragulus.		
OX	NCBI_TaxID=9849;		
EN	[1]		
EP	SEQUENCE FROM N.A.		
RX	MEDLINE=21347458; PubMed=11453981;		
RA	Bruckelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,		
RA	Warmeis H.W., Beintema J.J.;		
RA	"Secretory ribonucleases in the primitive ruminant chevrotain		
RT	(Tragulus javanicus).";		
RL	Eur. J. Biochem. 268:3890-3897(2001).		
CC	-i- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.		
DR	EMBL; AJ271299; CAC24723.1; -.		
DR	HSSP; P00656; 1LSQ.		
DR	GO; GO:0004519; F:endonuclease activity; IEA.		
DR	GO; GO:0016787; F:hydrolase activity; IEA.		
DR	GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.		
DR	InterPro; IPR001427; RNaseA.		
DR	Pfam; PF00074; rnaseA; 1.		
DR	PRINTS; PR00794; RIBONUCLEASE.		
DR	ProDom; PD000535; RNaseA; 1.		
DR	SMART; SM00092; RNase PC; 1.		
DR	PROSITE; PS00127; RNASE PANCREATIC; 1.		
KW	Endonuclease; Hydrolase; Nuclease; Signal.		
FT	NON TER 1		
FT	SIGNAL <1 19		POTENTIAL.
FT	CHAIN 20 170		BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE.
SQ	SEQUENCE 170 AA; 18832 MW; ABCE7E1E549AA0 CRC64;		
Query Match			
Best Local Similarity 21.2%; Score 128; DB 6; Length 170;			
Matches 40; Conservative 18; Mismatches 46; Indels 20; Gaps 7			
Qy	5	ATFOQKH-----INTPIIONTILDNNIYIVGGCKRVNTFISSATTVKAICT-----	53
Db	25	AKFRQHLDAAGSSINSN-YCNLMKRR-KMTHGRCKPNTFIHESLEDVKAICSEKNT	82
Qy	54	--GVINLVLSITRFRQNTCTRTSITRPP-CPYSSRTETNYICVKCN--QYPVHFAGI	107
Db	83	CKXGQPNCHQSNST-MNITDCRQTGGSKYPNCAYKTOKYIIVACEGTPSPVHFDS	141
Qy	108	GRCP 111	
Db	142	AVLP 145	
RESULT 15			
Q80Z85	PRELIMINARY;	PRT;	144 AA.
ID	Q80Z85		
AC	Q80Z85;		
DT	01-JUN-2003 (TReMBLrel. 24, Created)		
DT	01-JUN-2003 (TReMBLrel. 24, Last sequence update)		
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)		
DE	Angiogenin-4.		
GN	ANG4.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxID=10090;		
EN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=NMRI;		
RX	MEDLINE=22493143; PubMed=12548285;		

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DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR GO: GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR Signal.
KW SIGNAL.
FT CHAIN 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14804 MW; APEBFD67D266C7C2 CRC64;

Query Match 35.5%; Score 214.5; DB 13; Length 128;
Best Local Similarity 38.4%; Pred. NO. 8.2e-17;
Matches 43; Conservative 20; Mismatches 40; Indels 9; Gaps 4

Qy 2 QNWATFOQKHILNT-PIICNTILDNNIYIVGGQCKRVNTRFISSATTVKAICTGV-INLN 59
Db 24 QQWDTFOKKHLDTTKKVKCDVEMKALF----DCKKNTFIIFAPRPVQALCKRKIKNTN 79

Qy 60 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKENQYVPHFAGIGRCP 111
Db 80 VLSRDVYFLPQCNKKL---PCHYRLDGSNTWICLTCKMELPIHFAGVGKCP 128

RESULT 13
Q9W738 PRELIMINARY; PRT; 169 AA.
AC Q9W738;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FRL2 protein.
DE GN FRL2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96069863; PubMed=7585965;
RA Kinoshita N., Minshull J., Kirschner M.W.;
RT "The identification of two novel ligands of the FGF receptor by a
RT yeast screening method and their activity in Xenopus development.";
RL Cell 83:621-630(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Kinoshita N., Kirschner M.W.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
EMBL: AF159166; AAD41901.1; -.
DR HSP; P00656; ILSO.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR GO: GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;

Query Match 26.6%; Score 161; DB 13; Length 169;
Best Local Similarity 39.3%; Pred. NO. 1.6e-10;
Matches 44; Conservative 10; Mismatches 50; Indels 8; Gaps 6

Qy 2 QNWATFOQKHIL--NTPICN--TILDNNIYIVGGQCKRVNTRFI--ISSATTVKAICTGVIN 57
Db 28 QNTINAFMEKHIVKEGAETNCNTQIKDRNIRF--KNNCKFRNTFIHDTNGKKVKEMCAGIVK 86

Qy 58 LN-VLSTTRFQNLNCTRTSITPRP--CPYSSRTETNYICVKENQYVPHFAG 106
Db 87 STVISEKLLPLTDCLLMGRTPAPNCAYNQTRITGVINITCENNPVPHFAG 138

RESULT 14

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DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA

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RESULT 5
Q98SM1
ID Q98SM1 PRELIMINARY; PRT; 132 AA.
AC Q98SM1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21539506; PubMed=11683320;
EA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351208; AAK30254.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
FT SIGNAL
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match 73.5%; Score 444.5; DB 13; Length 132;
Best Local Similarity 77.3%; Pred. No. 3e-43;
Matches 85; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

Qy 2 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 60
Db 23 QDWTFQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINSNV 82

Qy 61 LSTTRFQINTCTRTSITPRPCYSRTETNYICVKCENQYVPHFAGIGRC 110
Db 83 LSTTRFQIXXTRFITSRPCYSSTKTNKICVKCENYVPHFAGIGKC 132

RESULT 6
Q9DF78
ID Q9DF78 PRELIMINARY; PRT; 132 AA.
AC Q9DF78;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE RC-RNaseL1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288642; AAG30414.2; -.

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DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
FT CHAIN
FT SIGNAL
SQ SEQUENCE 132 AA; 14625 MW; D8D9A517452PBE53 CRC64;

Query Match 61.5%; Score 372; DB 13; Length 132;
Best Local Similarity 64.9%; Pred. No. 6.5e-35;
Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;

Qy 2 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 59
Db 22 QNWAFKEKHITSIDCNTIMDKAIYVGGCKERNFTFISSDNVKAICSGVSPDRK 81

Qy 60 VLSTTRFQINTCTRTSITPRPCYSRTETNYICVKCENQYVPHFAGIGRC 110
Db 82 ELSTTSFKLNTCIRDSITPRPCYPHSPDNNKICVKCKQLPVHFGVIGKC 132

RESULT 7
Q918V8
ID Q918V8 PRELIMINARY; PRT; 127 AA.
AC Q918V8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Onconase variant rapR1 precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure."
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76935.1; -.
DR PIR; A39035; A39035.
DR HSSP; P22069; 1ONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
FT SIGNAL
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 45.9%; Score 277.5; DB 13; Length 127;
Best Local Similarity 48.6%; Pred. No. 4.6e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

Qy 2 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 59
Db 24 QDWLTFQKHINTTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 79

Qy 60 VLSTTRFQINTCTRTSITPRPCYSRTETNYICVKCENQYVPHFAGIGRC 110
Db 80 VLATSEFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFGVGHG 127

```

RA	Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT	"Rapid diversification of RNase A superfamily ribonuclease from the
RL	bullfrog, Rana catesbeiana.";
J. Mol. Evol.	53:31-38(2001)."
EMBL:	AF351210; AAK30256.1; -.
HSSP:	P11916; 1BC4.
DR	GO: GO:0003576; F:nucleic acid binding; IEA.
DR	GO: GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR	InterPro: IPR001427; RNaseA.
DR	Pfam: PF00074; rnasea; 1.
DR	ProDom: PD000535; RNaseA; 1.
DR	SMART: SM00092; RNase_Pc; 1.
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW	Signal.
FT	SIGNAL.
SQ	SEQUENCE 133 AA; 14615 MW; C87B5B236B26E54E CRC64;
	Query Match 78.4%; Score 474.5; DB 13; Length 133;
	Best Local Similarity 77.5%; Pred.No.1.1e-46;
	Matches 86; Conservative 12; Mismatches 12; Indels 1; Gaps 1;
QY	2 QNWATFOQKHINTPII-CNTILDNNIIYIVGGCKRWVFIISSTAVKAICTGVINLVN 60
Db	23 QNWATFOQKHINTTSINCINMNSLIYVGGCKKVNTFIASSATTVKGICSGVTDKV 82
QY	61 LSTRFQLMTCTRTSITPRPCPYSSSTETNYICVKCENQYPVHFAGIGRCP 111
Db	83 LSSTKFQDLICTRIFFTPRCPPYSSSTETNYICVKCENQYPVHFAGIGQCP 133
RESULT 4	
ID	Q98SL8 PRELIMINARY; PRT; 133 AA.
AC	Q98SL8;
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	RNase A-type ribonuclease rc218 precursor.
OS	Rana catesbeiana (Bull frog).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX	NCEI_TaxID=8400;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21539506; PubMed=11683320;
RT	Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RA	"Rapid diversification of RNase A superfamily ribonuclease from the
RL	bullfrog, Rana catesbeiana.";
J. Mol. Evol.	53:31-38(2001)."
EMBL:	AF351211; AAK30257.1; -.
HSSP:	P11916; 1BC4.
DR	GO: GO:0003576; F:nucleic acid binding; IEA.
DR	GO: GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR	InterPro: IPR001427; RNaseA.
DR	Pfam: PF00074; rnasea; 1.
DR	ProDom: PD000535; RNaseA; 1.
DR	SMART: SM00092; RNase_Pc; 1.
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW	Signal.
FT	SIGNAL.
SQ	SEQUENCE 133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
	Query Match 77.3%; Score 467.5; DB 13; Length 133;
	Best Local Similarity 75.7%; Pred.No.6.7e-46;
	Matches 84; Conservative 14; Mismatches 12; Indels 1; Gaps 1;
QY	2 QNWATFOQKHINTPII-CNTILDNNIIYIVGGCKRWVFIISSTAVKAICTGVINLVN 60
Db	23 QNWATFOQHINTTSINCINMNSLIYVGGCKKVNTFIASSATTVKGICSGVTDKV 82
QY	61 LSTRFQLMTCTRTSITPRPCPYSSSTETNYICVKCENQYPVHFAGIGRCP 111
Db	83 LSSTKFQDLICTRIFFTPRCPPYSSSTETNYICVKCENQYPVHFAGIGQCP 133

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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 31.566 Seconds

(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-21

Perfect score: 605

Sequence: 1 QNWATFOQKHINTPIICN.....ICVKCENQYVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	554.5	91.7	133	13	Q98SM0 rana catesb
2	483.5	75.9	132	13	Q98SM2 rana catesb
3	474.5	78.4	133	13	Q98SL9 rana catesb
4	467.5	77.3	133	13	Q98SL8 rana catesb
5	444.5	73.5	132	13	Q98SM1 rana catesb
6	372	61.5	132	13	Q98DF78 rana catesb
7	277.5	45.9	127	13	Q918V8 rana pipien
8	273.5	45.2	127	13	Q98UVX5 rana pipien
9	243	40.2	129	13	Q98DFY6 rana pipien
10	225.5	37.3	128	13	Q98DFX8 rana catesb
11	223.5	36.9	128	13	Q98DFY7 rana catesb
12	214.5	35.5	128	13	Q98DFX5 rana catesb
13	161	26.6	169	13	Q9W738 xenopus lae
14	128	21.2	170	6	Q98EC1
15	127.5	21.1	144	11	Q80Z85 mus musculus
16	127.5	21.1	153	11	Q80XS4 mus musculus

17	123.5	20.4	147	6	Q7YRJ6	Q7YRJ6 balaena mys
18	122	20.2	146	6	Q861Y5	Q861Y5 colobus gue
19	121.5	20.1	116	6	Q9TVC0	Q9TVC0 sus scrofa
20	121.5	20.1	163	6	Q9BDC2	Q9BDC2 antilocapra
21	121	20.0	150	11	Q8VD94	Q8VD94 berylmys bo
22	119	19.7	150	11	Q8VD88	Q8VD88 rattus norv
23	118.5	19.6	144	6	Q9BH14	Q9BH14 antilocapra
24	118.5	19.6	147	6	Q7YRJ5	Q7YRJ5 tursiops tr
25	116.5	19.3	149	11	Q8K2T2	Q8K2T2 mus musculus
26	116.5	19.3	149	11	Q8C6G3	Q8C6G3 mus musculus
27	116	19.2	146	6	Q861Y4	Q861Y4 trachypithe
28	115	19.2	150	11	Q8VD92	Q8VD92 rattus exul
29	115	19.0	146	6	Q861Y3	Q861Y3 pygathrix r
30	115	19.0	146	6	Q861Y2	Q861Y2 pygathrix b
31	115	19.0	146	6	Q861Y1	Q861Y1 pygathrix a
32	113.5	18.8	152	11	Q8VD89	Q8VD89 rattus norv
33	111	18.3	148	11	Q8C6G3	Q8C6G3 mus musculus
34	110.5	18.3	124	6	Q95NE6	Q95NE6 bubalus bub
35	109.5	18.1	148	11	Q8C7E4	Q8C7E4 mus musculus
36	109.5	18.1	149	11	Q8VD95	Q8VD95 berylmys bo
37	109	18.0	124	6	Q9BEC2	Q9BEC2 tragulus ja
38	109	18.0	134	6	Q9BDB9	Q9BDB9 tragulus ja
39	108.5	17.9	152	11	Q8VD84	Q8VD84 rattus tiom
40	108.5	17.9	156	6	Q8SQ05	Q8SQ05 lagothrix l
41	107.5	17.8	119	6	Q9TV28	Q9TV28 eulemur ful
42	107.5	17.8	119	6	Q9TV30	Q9TV30 saguinus oe
43	106.5	17.6	156	6	Q8SQ06	Q8SQ06 ateles geof
44	105.5	17.4	142	6	Q9BEC3	Q9BEC3 tragulus ja
45	105.5	17.4	156	6	Q8SQ08	Q8SQ08 salmiri sci

ALIGNMENTS

RESULT 1

Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; R:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase PG; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;
1 22 POTENTIAL.

Query Match 91.7%; Score 554.5; DB 13; Length 133;

Best Local Similarity 92.8%; Pred. No. 6.6e-56;

Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 2 QNWATFOQKHINTPII-CNTILDNNIYVGCQRVNTFFIISATTVKAITGVINLV 60

DB 23 QNWATFOQKHINTPII-CNTILDNNIYVGCQRVNTFFIISATTVKAITGVINLV 82

Q9BEC1
ID Q9BEC1 PRELIMINARY; PRT; 170 AA.
AC Q9BEC1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Brain-type ribonuclease ribonuclease precursor (Fragment).
GN RNase B.
OS Tragus javanicus (Lesser Malay chevron)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;
OC Tragulidae; Tragulus.
OX NCBI_TaxID=9849;
RX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347458; PubMed=11453981;
RA Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,
RA Warmels H.W., Beintema J.J.;
RT "Secretory ribonucleases in the primitive ruminant chevrotain
RT (Tragus javanicus).";
RL Eur. J. Biochem. 268:3890-3897(2001).
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR EMBL; AJ271299; CAC24723.1; -.
DR HSSP; P00656; 1LSQ.
DR GO; GO:0004519; F:endonuclease activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR Endonuclease; Hydrolase; Nuclease; Signal.
KW NON TER 1
FT SIGNAL <1 19
FT CHAIN 20 170
FT SEQUENCE 170 AA; 18832 MW; AB6CE7E1E5549AA0 CRC64;
Query Match 21.6%; Score 131; DB 6; Length 170;
Best Local Similarity 33.1%; Pred. No. 2.8e-07;
Matches 41; Conservative 17; Mismatches 46; Indels 20; Gaps 7;

QY 5 ATFOCKH-----INTPIICNTIMNNIYVGGCKRVNTFISSATTVKAICT----- 53
DB 25 AKFRQHLDAAGNSINSN-YCNLMKKR-KMTHGRCKPVNTFIESLEDVKAICSEKNIT 82
QY 54 ---GVINMNVLTFRPQINTCTRTSITRP-CPYSSRTETNYICVKCN--QYPVHPAGI 107
DB 83 CKGQPNCHQSNST-MNITDCRQTGGSKYPNCAYKTSQKQKIIVACEGTPSPVPHFDGS 141
QY 108 GRCP 111
DB 142 AVLP 145

RA Hooper L.V., Stappenbeck T.S., Hong C.V., Gordon J.I.;
RT "Angiogenins: a new class of microbicidal proteins involved in innate
RT immunity.";
RL Nat. Immunol. 4:269-273(2003).
DR EMBL; AY219870; BAO62354.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SEQUENCE 144 AA; 16554 MW; 09808807C00224C1 CRC64;
Query Match 21.2%; Score 128.5; DB 11; Length 144;
Best Local Similarity 38.2%; Pred. No. 4.6e-07;
Matches 29; Conservative 13; Mismatches 29; Indels 5; Gaps 3;

QY 34 CKRVNTFISSATTVKAIC---TGVINMNV-LSTTRFQINTCTRTSITP-RPCPYSSRTE 88
DB 62 CKDWNTHGTTKKNRAICGKSGPYGENFRISNPFQITCTHRSRGPWPWPCGAFK 121
QY 89 TNYICVKCNQYPVHF 104
DB 122 FRYIVACEDGWPVHF 137
Search completed: May 11, 2004, 14:36:30
Job time : 36.6606 secs

RESULT 15
Q80285
ID Q80285 PRELIMINARY; PRT; 144 AA.
AC Q80285;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Angiogenin-4.
GN ANG4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI;
RX MEDLINE=22493143; PubMed=12548285;

RESULT 11
 Q9DFY7 ID Q9DFY7 PRELIMINARY; PRT; 128 AA.
 AC Q9DFY7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RC-RNase3 ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 RC MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog).";
 RL Nucleic Acids Res. 28:4097-4104(2000).
 DR EMBL; AF242554; AAG31440.2; -;
 DR HSSP; P22069; IONC.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR ProDom; PD000535; RNaseA; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 KW SIGNAL.
 FT SIGNAL.
 FT CHAIN 1 23 POTENTIAL.
 FT CHAIN 24 128 RC-RNase3 RIBONUCLEASE.
 SQ SEQUENCE 128 AA; 14517 MW; 2814986082E0587D CRC64;
 Query Match 36.6%; Score 221.5; DB 13; Length 128;
 Best Local Similarity 40.5%; Pred. No. 5.7e-18;
 Matches 45; Conservative 18; Mismatches 39; Indels 9; Gaps 4;
 Qy 3 NWATFOQKHINT-PIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGV-INNV 60
 Db 25 DWETFOKKHLDTKKVKCDVEMAKALF---DCKKNTFTIYALPGRVKALCKIRNTDV 80
 Qy 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCNQVPHFAGIGRCP 111
 Db 81 LSRDAFLLPQCDRIKL---PCHYKLSSTNTICITCNQLPIHFAGVGS 128
 RESULT 12
 Q9DFY5 ID Q9DFY5 PRELIMINARY; PRT; 128 AA.
 AC Q9DFY5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RC-RNase6 ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 RC MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog).";
 RL Nucleic Acids Res. 28:4097-4104(2000).
 DR EMBL; AF242556; AAG31442.2; -;
 DR HSSP; P22069; IONC.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR ProDom; PD000535; RNaseA; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 KW SIGNAL.
 FT SIGNAL.
 FT CHAIN 1 23 POTENTIAL.
 FT CHAIN 24 128 RC-RNase3 RIBONUCLEASE.
 SQ SEQUENCE 128 AA; 14517 MW; 2814986082E0587D CRC64;
 Query Match 36.6%; Score 221.5; DB 13; Length 128;
 Best Local Similarity 40.5%; Pred. No. 5.7e-18;
 Matches 45; Conservative 18; Mismatches 39; Indels 9; Gaps 4;
 Qy 3 NWATFOQKHINT-PIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGV-INNV 60
 Db 25 DWETFOKKHLDTKKVKCDVEMAKALF---DCKKNTFTIYALPGRVKALCKIRNTDV 80
 Qy 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCNQVPHFAGIGRCP 111
 Db 81 LSRDAFLLPQCDRIKL---PCHYKLSSTNTICITCNQLPIHFAGVGS 128
 RESULT 13
 Q9W738 ID Q9W738 PRELIMINARY; PRT; 169 AA.
 AC Q9W738;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE FRL2 protein.
 GN FRL2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96069863; PubMed=7585965;
 RA Kinoshita N., Minshull J., Kirschner M.W.;
 RT "The identification of two novel ligands of the FGF receptor by a
 yeast screening method and their activity in Xenopus development.";
 RL Cell 83:621-630(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kinoshita N., Kirschner M.W.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF159166; AAD41901.1; -;
 DR HSSP; P00856; ILSQ.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR ProDom; PD000535; RNaseA; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 SQ SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;
 Query Match 26.1%; Score 158; DB 13; Length 169;
 Best Local Similarity 38.7%; Pred. No. 2e-10;
 Matches 43; Conservative 10; Mismatches 50; Indels 8; Gaps 6
 Qy 3 NWATFOQKHII--NTPICN-TIMDNIIYVGQCKRVNTFI-SSATTVKAICTGVIN 58
 Db 29 NINAFMEKHIVKEGATNCQTIKDRNIRF-KNNCKFRNTFIHDTNGKKVKWCAGIVKS 87
 Qy 59 N-VLSTTRFQNLCTRTSITPRP--CPYSSRTETNYICVKCNQVPHFAG 106
 Db 88 TFVISKELLPLTDCLLMGRTARPPNCAYNQTRTTGTGVINITCENNYVPHFAG 138
 RESULT 14


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RESULT 5
Q98SM1
ID Q98SM1 PRELIMINARY; PRT; 132 AA.
AC Q98SM1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;
EX MEDLINE=21539506; PubMed=11583320;
RA Rosenberg H.F.; Zhang J.; Liao Y.-D.; Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351208; AAK30254.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNASE_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match 73.2%; Score 443.5; DB 13; Length 132;
Best Local Similarity 78.0%; Pred. No. 7.3e-44;
Matches 85; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

QY 3 NWATFOQKHINTPIL-CNTIMDNNIYVGGCKRVNTFISSATVKAICTGVINMNV 61
DB 24 DWFTFOQKHPTSSIDCNTIMDKIYVIRGCKKRVNTFISSATVKAICTGVINMNV 93

QY 62 STTRFQNTCTRTSITPRPCYSSTRTNYICVKCENQYPVHFAGIRC 110
DB 84 STTRFQXXTRTFTSITPRPCYSSTRTNYICVKCENQYPVHFAGIRC 132

RESULT 6
Q9DF78
ID Q9DF78 PRELIMINARY; PRT; 132 AA.
AC Q9DF78;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNaseL1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D.; Huang H.-C.; Leu Y.-J.; Wei C.-W.; Tang P.-C.; Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D.; Huang H.-C.; Leu Y.-J.; Wei C.-W.; Tang P.-C.; Wang S.-C.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF288642; AAG30414.2; -.

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DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNASE_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14625 MW; D8D9A517452FB53 CRC64;

Query Match 61.2%; Score 371; DB 13; Length 132;
Best Local Similarity 65.5%; Pred. No. 2.1e-35;
Matches 72; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

QY 3 NWATFOQKHINTPIL-CNTIMDNNIYVGGCKRVNTFISSATVKAICTGVINMNV 60
DB 23 NWAKFKKHITSSIDCNTIMDKIYVIRGCKKRVNTFISSATVKAICTGVINMNV 82

QY 61 LSTTRFQNTCTRTSITPRPCYSSTRTNYICVKCENQYPVHFAGIRC 110
DB 83 LSTTSFKLNTCTRTSITPRPCYPHPSPDNKIKVCKEQLPVHFVGVGKC 132

RESULT 7
Q918V8
ID Q918V8 PRELIMINARY; PRT; 127 AA.
AC Q918V8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase variant rap1 precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L.; Le S.-Y.; Newton D.L.; Maizel J.V. Jr.; Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure."
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76935.1; -.
DR PIR; A39035; A39035.
DR HSSP; P22069; 1ONG.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNASE_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14491 MW; B8511DCS407AB69B CRC64;

Query Match 45.6%; Score 276.5; DB 13; Length 127;
Best Local Similarity 49.1%; Pred. No. 2.2e-24;
Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 3 NWATFOQKHINTPIL-CNTIMDNNIYVGGCKRVNTFISSATVKAICTGVINMNV 60
DB 25 DWLTFQKHINTTRDVCNNIMSTNLF----HCKKNTFIYSRPEPVKAICKGIASKNV 80

QY 61 LSTTRFQNTCTRTSITPRPCYSSTRTNYICVKCENQYPVHFAGIRC 110
DB 81 LTTSEFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

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RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;

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QY      62 STRFOLNCTRTSITPRPCPYSSRRTETNYICVKCNOYPVHEAGIRCP 111
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OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 14:30:53 ; Search time 35.6606 Seconds

(without alignments)
982.106 Million cell updates/sec

Title: US-09-961-400-26

Perfect score: 606

Sequence: 1 MSNWATFOQKHINTPIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	555.5	91.7	133	Q98SM0	Q98sm0 rana catesb
2	482.5	79.6	132	Q98SM2	Q98sm2 rana catesb
3	473.5	78.1	133	Q98SL9	Q98sl9 rana catesb
4	466.5	77.0	133	Q98SL8	Q98sl8 rana catesb
5	443.5	73.2	132	Q98SM1	Q98sm1 rana catesb
6	371	61.2	132	Q9DF78	Q9df78 rana catesb
7	276.5	45.6	127	Q918V8	Q918v8 rana pipien
8	272.5	45.0	127	Q9UVX5	Q9uvx5 rana pipien
9	241	39.8	129	Q9DFY6	Q9dfy6 rana catesb
10	224.5	37.0	128	Q9DFY8	Q9dfy8 rana catesb
11	221.5	36.6	128	Q9DFY7	Q9dfy7 rana catesb
12	212.5	35.1	128	Q9DFY5	Q9dfy5 rana catesb
13	158	26.1	169	Q9W738	Q9w738 xenopus lae
14	131	21.6	170	Q9BEC1	Q9bec1 tragulus ja
15	128.5	21.2	144	Q8QZ85	Q8qz85 mus musculus
16	128.5	21.2	153	Q8QXS4	Q8qxs4 mus musculus

17	127.5	21.0	147	6	Q7YRJ6	Q7yrrj6 balaena mys
18	126	20.8	150	11	Q8VD94	Q8vd94 berylmys bo
19	125.5	20.7	163	6	Q9BDC2	Q9bdc2 antilocapra
20	124.5	20.5	116	6	Q9TVC0	Q9tvc0 sus scrofa
21	124	20.5	150	11	Q8VD88	Q8vd88 rattus norv
22	123.5	20.4	146	6	Q861Y4	Q861y4 trachypithe
23	122.5	20.2	144	6	Q9BH14	Q9bh14 antilocapra
24	122.5	20.2	146	6	Q861Y3	Q861y3 pygathrix r
25	122.5	20.2	146	6	Q861Y2	Q861y2 pygathrix b
26	122.5	20.2	146	6	Q861Y1	Q861y1 pygathrix a
27	121.5	20.0	147	6	Q7YRJ5	Q7yrrj5 tursiops tr
28	121	20.0	146	6	Q861Y5	Q861y5 colobus gue
29	120.5	19.9	149	11	Q8K2Y2	Q8k2t2 mus musculu
30	120.5	19.9	149	11	Q8CGG3	Q8cgg3 mus musculu
31	120	19.8	150	11	Q8VD92	Q8vd92 rattus exul
32	116.5	19.2	152	11	Q8VD89	Q8vd89 rattus norv
33	114.5	18.9	124	6	Q9SNE6	Q9sne6 bubalus bub
34	112.5	18.6	148	11	Q8C7E4	Q8c7e4 mus musculu
35	112.5	18.6	149	11	Q8VD95	Q8vd95 berylmys bo
36	112	18.5	134	6	Q9BDB9	Q9bdb9 tragulus ja
37	111.5	18.4	152	11	Q8VD84	Q8vd84 rattus tiom
38	111.5	18.4	156	6	Q8SQ05	Q8sq05 lagothrix l
39	111	18.3	148	11	Q8C6G3	Q8c6g3 mus musculu
40	110.5	18.2	119	6	Q9TV28	Q9tv28 eulemur ful
41	110.5	18.2	119	6	Q9TV30	Q9tv30 saguinus oe
42	109.5	18.1	142	6	Q9BEC3	Q9bec3 tragulus ja
43	109.5	18.1	156	6	Q8SQ06	Q8sq06 ateles geof
44	109	18.0	124	6	Q9BEC2	Q9bec2 tragulus ja
45	108.5	17.9	156	6	Q8SQ08	Q8sq08 saimiri sci

ALIGNMENTS

RESULT 1

Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38 (2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL. 1 22 POTENTIAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 91.7%; Score 555.5; DB 13; Length 133;

Best Local Similarity 94.5%; Pred. No. 6.3e-57;

Matches 104; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 3 NWATFOQKHINTPII-CNTIMDNNIYVGGCKRVNTFIISATTVKAICTGVINNV 61

DB 24 NWATFOQKHINTPII-CNTIMDNNIYVGGCKRVNTFIISATTVKAICTGVINNV 83

RA Q9BEC1 PRELIMINARY; PRT; 170 AA.
 AC Q9BEC1;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Brain-type ribonuclease ribonuclease precursor (fragment).
 GN RNASE B.
 OS Tragus javanicus (Lesser Malay chevron)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;
 OC Tragulidae; Tragulus.
 OX NCBI_TaxID=9849;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2137459; PubMed=11453981;
 RA Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,
 RA Warmels H.W., Beintema J.J.;
 RT "Secretory ribonucleases in the primitive ruminant chevrotain
 (Tragus javanicus).";
 RL Eur. J. Biochem. 268:3890-3897(2001).
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR EMBL; AJ271299; CAC24723.1; -.
 DR HSP; P00656; ILSQ.
 DR GO; GO:0004519; F:endonuclease activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR PRINTS; PR00794; RIBONUCLEASE.
 DR ProDom; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 KW Endonuclease; Hydrolase; Nuclease; Signal.
 FT NON TER 1
 FT SIGNAL <1 19 POTENTIAL.
 FT CHAIN 20 170 BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE.
 SQ SEQUENCE 170 AA; 18832 MW; AB6CE7E1E5549AA0 CRC64;

Query Match 21.8%; Score 131; DB 6; Length 170;
 Best Local Similarity 33.1%; Pred. No. 2.8e-07;
 Matches 41; Conservative 17; Mismatches 46; Indels 20; Gaps 7;
 QY 4 ATFOQKH-----INTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICT-----52
 DB 25 AKFRQHLDAAGSSINSN-YCNLMKKR-KMTHGRCKPNTFIHESLEDVKAICSEKNIT 82
 QY 53 ---GVINMNVLTSTRFQNTCTRTSITPRP-CPYSSRTETNYICVKCN--QYPVHPAGI 106
 DB 83 CKNGQPNCHQSNST-MNITDCROTGGSKYPNCAYKTSOKYIIIVACEGTSPVPVHFDGS 141
 QY 107 GRCP 110
 DB 142 AVLP 145

RESULT 15
 Q80Z85 PRELIMINARY; PRT; 144 AA.
 ID Q80Z85
 AC Q80Z85;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Angiogenin-4.
 GN ANG4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI;
 RX MEDLINE=22493143; PubMed=12548285;

Hooper L.V., Stappenbeck T.S., Hong C.V., Gordon J.I.;
 "Angiogenins: a new class of microbicidal proteins involved in innate immunity.";
 RL Nat. Immunol. 4:269-273(2003).
 DR EMBL; AY219870; AA062354.1; -.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR PRINTS; PR00794; RIBONUCLEASE.
 DR ProDom; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 SQ SEQUENCE 144 AA; 16554 MW; 0980807C00224C1 CRC64;

Query Match 21.4%; Score 128.5; DB 11; Length 144;
 Best Local Similarity 38.2%; Pred. No. 4.6e-07;
 Matches 29; Conservative 13; Mismatches 29; Indels 5; Gaps 3;
 QY 33 CKRVNTFISSATTVKAIC---TGVINMNV-LSTTRFQNTCTRTSITP-RPCPYSSRTE 87
 DB 62 CKDVNTFIHGCKKNIRAIKCGKSGPYGENFRISNPFQITTCRSGSPWPPCGYRAFKD 121
 QY 88 TNYICVKCNQYEVHF 103
 DB 122 FRXIVACEDGWPVHF 137

Search completed: May 11, 2004, 14:36:29
 Job time : 36.3394 secs

RESULT 14


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RESULT 8
Q8UVX5 PRELIMINARY; PRT; 127 AA.
ID Q8UVX5;
AC Q8UVX5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase precursor.
OS Rana pipiens (Northern leopard frog).
GN Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT "Rana pipiens onconase genomic DNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -.
DR PIR; A39035; A39035.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CPEEF3 CRC64;

Query Match 45.3%; Score 272.5; DB 13; Length 127;
Best Local Similarity 49.1%; Pred. No. 6.2e-24;
Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 2 NWATFOQKHINT-PIICNTIMNNIYVGQCKRVNTFIISATVKAICTGVI-NMNV 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 25 DWLTFQKKHLITRDVDCNIMSTLNF---HCKDKNTFIYSRPPVKAICKGIIASKNV 80

QY 60 LSTTRFQMLTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 109
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 81 LTTSEFYLSDC---NVTSPCKYKLLKSKTNKFCVTCEQAPVHFVGVGSC 127

RESULT 9
Q9DFY6 PRELIMINARY; PRT; 129 AA.
ID Q9DFY6;
AC Q9DFY6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242555; AAG31441.2; -.
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 129 AA; 14724 MW; 826A62862B10ABDA CRC64;

Query Match 40.1%; Score 241; DB 13; Length 129;
Best Local Similarity 42.9%; Pred. No. 3e-20;
Matches 48; Conservative 24; Mismatches 30; Indels 10; Gaps 5;

QY 2 NWATFOQKHINT-PIICNTIMNNIYVGQCKRVNTFIISATVKAICTGVI-NMNV 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 25 DWATFKKKHLITRDVDCNLMPTSLF---DCKDKNTFIYSLPGPVKALCRGVIFSADV 80

QY 60 LSTTRFQMLTCTRTSITPR-PCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 81 LSNSEFYLAEC---NVRPKPKCKYKLLKSSNRICIRCEHELPHVHPAGVGICP 129

RESULT 10
Q9DFY8 PRELIMINARY; PRT; 128 AA.
ID Q9DFY8;
AC Q9DFY8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242555; AAG31439.1; -.
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 37.4%; Score 224.5; DB 13; Length 128;
Best Local Similarity 39.6%; Pred. No. 2.5e-18;
Matches 44; Conservative 20; Mismatches 38; Indels 9; Gaps 4;

QY 2 NWATFOQKHINT-PIICNTIMNNIYVGQCKRVNTFIISATVKAICTGVI-NMNV 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 25 NWETFKKKHLITRDVDCDAEMKKALF-----DCKDKNTFIYARPGRVQALCKNIIKXNV 80

QY 60 LSTTRFQMLTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 81 LSTDFEYLSDCNRKIL---PCHYKLLKSSNTICITCENKLPVHFVAVEBCP 128
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[illegible]

Db 84 SSKTKQLDICTRIFITPRPCPYSSRTETNYICVKCENQYVHFAGIGQCP 133

RP SEQUENCE FROM N. A.
RX MEDLINE=21539506; PubMed=11683320;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 14:30:53 ; Search time 35.3394 Seconds
(without alignments)
982.106 Million cell updates/sec

Title: US-09-961-400-24

Perfect score: 601

Sequence: 1 SNWATFOQKHINTPIICNT.....ICVKCNQYVPHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rhodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	555.5	92.4	133	13	Q98SM0 rana catesb
2	482.5	80.3	132	13	Q98SM2 rana catesb
3	473.5	78.8	133	13	Q98SL9 rana catesb
4	466.5	77.6	133	13	Q98SL8 rana catesb
5	443.5	73.8	132	13	Q98SM1 rana catesb
6	371	61.7	132	13	Q9DF78 rana catesb
7	276.5	46.0	127	13	Q918V8 rana pipien
8	272.5	45.3	127	13	Q8UVX5 rana pipien
9	241	40.1	129	13	Q9DFY6 rana pipien
10	224.5	37.4	128	13	Q9DFY8 rana catesb
11	221.5	36.9	128	13	Q9DFY7 rana catesb
12	212.5	35.4	128	13	Q9DFY5 rana catesb
13	158	26.3	169	13	Q9W738 xenopus lae
14	131	21.8	170	6	Q9BEC1 tragus ja
15	128.5	21.4	144	11	Q8OZ85 mus musculus
16	128.5	21.4	153	11	Q8OXS4 mus musculus

17	127.5	21.2	147	6	Q7YRJ6
18	126	21.0	150	11	Q8VD94
19	125.5	20.9	163	6	Q9BDC2
20	124.5	20.7	116	6	Q9TVC0
21	124	20.6	150	11	Q8VD88
22	123.5	20.5	146	6	Q861Y4
23	122.5	20.4	144	6	Q9BH14
24	122.5	20.4	146	6	Q861Y3
25	122.5	20.4	146	6	Q861Y2
26	122.5	20.4	146	6	Q861Y1
27	121.5	20.2	147	6	Q7YRJ5
28	121	20.1	146	6	Q861Y5
29	120.5	20.0	149	11	Q8K2T2
30	120.5	20.0	149	11	Q8G6G3
31	120	20.0	150	11	Q8VD92
32	116.5	19.4	152	11	Q8VD89
33	114.5	19.1	124	6	Q95NE6
34	112.5	18.7	148	11	Q8C7E4
35	112.5	18.7	149	11	Q8VD95
36	112	18.6	134	6	Q9BDB9
37	111.5	18.6	152	11	Q8VD84
38	111.5	18.6	156	6	Q8SQ05
39	111	18.5	148	11	Q8C6E3
40	110.5	18.4	119	6	Q9TW28
41	110.5	18.4	119	6	Q9TV30
42	109.5	18.2	142	6	Q9BEC3
43	109.5	18.2	156	6	Q8SQ06
44	109	18.1	124	6	Q9BEC2
45	108.5	18.1	156	6	Q8SQ08

ALIGNMENTS

RESULT 1

Q98SM0 PRELIMINARY; PRT; 133 AA.
 ID Q98SM0
 AC Q98SM0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE RNase A-type ribonuclease rc208 precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 NC NCHI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21539506; PubMed=11683320;
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 RT bullfrog, Rana catesbeiana.";
 RL J. Mol. Evol. 53:31-38(2001).
 DR EMBL; AF351209; AAK30255.1; -.
 DR HSSP; P11916; 1BC4.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF000074; rnasea; 1.
 DR ProDom; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase PC; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 92.4%; Score 555.5; DB 13; Length 133;
 Best Local Similarity 94.5%; Pred. No. 6e-57;
 Matches 104; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 QY 2 NNATFOQKHINTPII-CNTIMDNNTIYVGQCKRVNTFIISATTVAICTGVINNVNVL 60
 DB 24 NNATFOQKHINTPII-CNTIMDNNTIYVGQCKRVNTFIISATTVAICTGVINNVNVL 83